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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                      Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                  Score
    protein search, using sw model
                                                                                                                                                                                                                                                                                Match
                                                                                                                                                                                                                                                                                                         Query
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111:
12:
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1: /SIDS1/gcgd=+=-/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT: *
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT: *
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT: *
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT: *
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT: *
10: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT: *
11: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT: *
12: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT: *
13: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT: *
14: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT: *
15: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT: *
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18: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT: *
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT: *
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT: *
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT: *
23: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT: *
24: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT: *
25: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT: *
26: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT: *
27: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT: *
28: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT: *
    July 30, 2002, 14:47:39; Search time 53.42 Seconds (without alignments) 95.646 Million cell updates/sec
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Gapop 10.0 , Gapext 0.
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227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
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Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
                                                                                                                                                                                                                                                                                Length
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    173
553
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  AAW28307
AAU35204
AAP70176
AAR58858
AAR49141
AAW66928
AAW106928
AAW106918
AAW21983
AAW21983
AAY51231
AAY51231
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                                                                                    Staphylococcus aur
Enterococcus faeca
Sequence of Newcas
Newcastle Disease
Newcastle disease
Newcastle disease
                                                                                                                                                                                                                                                                             Description
                      Seq ID No: 14 of U
Protein encoded by
Newcastle disease
fusion (F) pro
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Mutant uracil	AAW21819	18	313		51	45
Thymine DNA glycos	AAW21816	18	313	2	51	44
Cytosine DNA glyco	AAW21815	18	313	2	51	43
Uracil DNA glycos	AAW21814	18	313	2	51	42
Mutant uracil	AAW21825	18	313	2	51	41
Mutant uracil	AAW21824	18	313	,2	51	40
Mutant uracil	AAW21822	18	313	2		39
Mutant uracil	AAW21821	18	313	2		38
Human colon cancer	AAG74939	22	292	22.5	45	37
Staphylococcus aur	AAU37294	22	220			36
Novel human	ABG07038	22	3076	Ν.	٢	ω 51
	ABG18288	22	2737	22.7	<u>, , , , , , , , , , , , , , , , , , , </u>	34
Novel human	ABG10345	22	591	22.7	Ξ.	ω ω
E. coli growth and	AAG98991	22	306	22.7	51.5	32
	AAB15918	21	306	22.7	۳.	31
Escherichia coli	AAG98329	22	257	22.7	۲.	30
Novel human diagno	ABG17731	22	177	22.7	51.5	29
	AAY51636	21	516	ν.		28
M. jannaschii	AAY52007	21	516			27
Human protein	AAM78621	22	382	Ν.		26
	AAM79605	22	381		52	25
	AAM79604	22	381	2.		24
Human protein	AAM78620	22	365	'n		23
Novel human diagno	ABG28821	22	148	2	52	22
L.lactis branched	AAR54214	15	513	u.		21
Arabidopsis thalia	AAG57201	21	96	ω.	53	20
Newcastle disease	AAR10065	12	553	ω.		19
Haemophilus	AAB23860	21	2411	w	54	18
Haemophilus	AAR99393	17	2353	ω.	54	17
Monellin	AAR34192	14	97	ω.	54	16
Monellin	AAR35757	14	96	w	54	15
Arabidopsis	AAG44398	21	$\vdash$		54.5	14
Arabidopsis		21	508	24.0	4.	13
<ol> <li>S. epidermidis</li> </ol>	AAG82132	22	œ	24.2	55	12

## ALIGNMENTS

RESULT AAW28307 ACC CONTRACTOR OF THE TENTON O Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome; Misc-difference 132 Staphylococcus aureus protein of unknown function. 01-SEP-1998 (first entry) AAW28307 standard; Protein; 173 AA (SMIK ) SMITHKLINE BEECHAM CORP. Staphylococcus aureus 20-FEB-1996; 19-FEB-1997; 21-AUG-1997. WO9730070-A1. Misc-difference 123 toxic shock syndrome. 96US-0011888. 97WO-US02318 Location/Qualifiers /note= "X is not defined in the specification" /note= "X is not defined in the specification"

Black MT,

Burnham MK, Hodgson JE,

Knowles DJC,

Nicholas RO

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RESULT
AAU35204
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Best Local
                                                                                                                                      21 - MAR - 2000;
23 - MAY - 2000;
26 - MAY - 2000;
23 - OCT - 2000;
23 - OCT - 2000;
27 - NOV - 2000;
16 - FEB - 2001;
           WPI; 2001-611495/70.
N-PSDB; AAS53063.
                                                                                                                                                                                                                                                                                                                                  WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown function. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coll. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 597-598; 989pp; English.
                                                                                                                                                                                                                                                                     21-MAR-2001;
                                                                                                                                                                                                                                                                                                   27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis cellular proliferation protein #491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU35204 standard; Protein; 939 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to isolate antimicrobial compounds, and in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT84204.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU35204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a Staphylococcus aureus protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aureus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-424969/39
                                                         Haselbeck R,
Yamamoto RT,
                                                                                                          (ELIT-) ELITRA PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                      2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                     2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                         Ohlsen
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R₩,
                                                                        KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenberg M,
                                                                          Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; 1
Pred. No. 3
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                                                                          Wall D,
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3.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 173;
                                                                            Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                            Carr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klabsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets of antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC programmes. The antisense nucleic acid sequence is also useful to screen CC essential prokaryotic cellular proliferation protein.

CC wide variety of organisms. The present sequence represents an CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Wipo at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                             Newcastle disease virus gene clones - comprise polynucleotide(s) encoding the HN and/or F protein of Newcastle disease virus {\tt RNA}
                                                                                                                                                                                                                                                                                                                                 01-JUL-1987
                                                                                                                                                                                                                                                                                                                                                                   EP227414-A.
                                                                                                                                                                                                                                                                                                                                                                                                   Newcastle Disease Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids \cdot
           Example; pages 11-16; 22pp; English
                                                                                                     N-PSDB;
                                                                                                                      WPI; 1987-179630/26
                                                                                                                                                        Bingham RW,
                                                                                                                                                                                        (NATR ) NATIONAL RES DEV CORP
                                                                                                                                                                                                                                            15-JUL-1986;
18-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Epitope; probe; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of Newcastle Disease Virus (NDV) F polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP70176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP70176 standard; protein; 553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Seq ID No 10797; 511pp; English.
                                                                                                                                                                                                                                                                                               16-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 idmdtpfeelpadqqeiilngsgeknfhfhyen 362
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                                                                                                     AAN70261
                                                                                                                                                        Chambers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                        86US-0885765.
85GB-0031147.
86GB-0009037.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.7%;
                                                                                                                                                        ۳,
                                                                                                                                                        Emmerson PT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB . 45;
                                                                                                                                                        Millar NS
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Matches

16;

Conservative

Query Match
Best Local Similarity

24.4%;

Score 55.5; Pred. No. 29;

DB 20; 15;

Mismatches

Indels Length 553;

5

Gaps

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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An artificial polynucleotide, encoding an HN and/or F polypeptide of Newcastle Disease Virus (NDV) DNA, a bioprecursor of the polypeptide, or an epitopic portion of the polypeptide or an artificial nucleotide complementary to the polynucleotide are claimed. The polynucleotides are useful for preparing a probe for extracting similar genes from a gene library or for identifying the prescence of NDV virons in a sample obtd. from poultry.
                                      Newcastle Disease Virus (NDV) HN and F genes were inserted as a Sfil fragment into the homology vector 443-88.8 at the unique sfil site. The NDV HN and F genes were inserted in the same transcriptional orientation as the ORF in the parental homology vector. The sequence of Sfil fragment is in AAQ68943/R58858/AAR58859. The inserted Sfil fragment has the following structure: Junction A - Fragment 1 (HN, AAs 2-577) - Junction B - Fragment 2 (F, AAs 1-553) - Junction C - Fragment 3 (BRS32) - Junction D. Fragment 1 is approx. 1811 bp AvaII to Nael fragment of the NDV HN CDNA clone (Bl strain). Fragment 2 is an approx 1812 bp BamHI to PstI fragment of the full length NDV F CDNA (Bl Strain). Fragment 3 is an approx 235 bp PstI and Scal fragment of the plasmid pBR322.
                                                                                                                                                                                                                                                          Disclosure; Page 70-72; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SfiI fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newcastle Disease Virus F gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR58858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR58858 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence '
                                                                                                                                                                                                                                                                                                        New recombinant fowl pox virus for use in vaccines - genes expressing antigens of Newcastle disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                 (JAPG ) NIPPON ZEON KK. (SYTR ) SYNTRO CORP.
                             AAQ68947,Q68948.
                                                                                                                                                                                                                                                                                           infectious bronchitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 tlrlsgefdatyqknisiqdsqviitgnldistelgnvnnsisnalnk 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 TLSLKNDF-----KEIKTDELEIJIGGSGSLSTFFRLFNRSFTQALGK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                     1994-294007/36
                                                                                                                                                                                                                                                                                                                                                        AAQ68943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newcastle Disease Virus; F gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0024156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-US01826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                        opt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Sequence

553 AA;

AAW06828

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                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                  AAW06828
                                                                                                                             Matches
                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                          AAQ70570 is the Sfil fragment insert in Homology Vector 502-26.22 contg. Newcastle disease virus (NDV) HN and F genes. The Structure of the fragment is: 5'- Junction A - Fragment 1 (NDV HN AAS 2-57) - Junction B - Fragment 2 (NDV F AAS 1-553) - Junction C - Fragment 3 (pBR322) - Junction D - 3'. Fragment 1 is Avail to Nael fragment of the full length NDV HN CDNA clone (Bl strain). Fragment 2 is BamHI to PstI fragment of the full length NDV F cDNA (Bl strain). Fragment 3 is a PstI and Scal fragment of pBR322. The structures of the Junctions A, B, C and D are given in AAQ70552, AAQ70553, AAQ70554 and AAQ70555 respectively.
AAW06828 standard; Protein; 553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant fowl pox viruses – useful as vaccines against fowl pox virus, Newcastle Disease Virus and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cochran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9419015-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Newcastle disease virus F gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR49141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR49141 standard; Protein;
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 79-81; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newcastle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                              laryngotracheitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYTR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 tlrlsgefdvtyqknisiqdsqviitgnldistelgnvnnsisnalnk 480
                                                                       433 tlrlsgefdvtyqknisiqdsqviitgnldistelgnvnnsisnalnk 480
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TLSLKNDF-----KEIKTDELEIIIGGSGSLSTFFRLFNRSFTQALGK
                                                                                                 4 TLSLKNDF-----KEIKTDELEIIIGGSGSLSTFFRLFNRSFTQALGK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ഗ
                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1994-294008/36
                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ70570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease virus;
                                                                                                                                                                                                  553 AA;
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9308-0024156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US02252
                                                                                                                                        24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553 AA
                                                                                                                                         Score 55.5;
Pred. No. 29;
                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SfiI; vector 502-26.22
                                                                                                                                                         DΒ
                                                                                                                             20;
                                                                                                                                                       Length
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                          553;
                                                                                                                             5
                                                                                                                             Gaps
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SXXCCCCCCCCCXXXXIII
RESULT
AAWIJO691
ID AAWI
XX
AC AAWI
XX
DT 05-)
XX
DE Newo
XX
KW immu
KW immu
                                                                                                                                                                                                           В
                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Turkey herpes Virus; recombinant virus; vaccine; prophylaxis; immunisation; avian virus; infectious bronchitis virus; infectious bursal disease virus; Newcastle disease virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-1994;
09-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Newcastle disease virus F gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                   sequence encoding a cytokine inserted into a XhoI site within an EcoRI #9 genomic fragment, where the cytokine can be expressed in host cells infected with the virus can be used in vaccines to protect turkeys against avian viruses. The recombinant viruses can be used for immunising birds against infectious bronchitis virus (IBV), infectious bursal disease virus (IBV), where the control of the virus (MDV) infectious laryngotracheitis virus (IIV) and Newcastle disease virus (MDV). They may also be used in multivalent vaccines to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant turkey herpes viruses contg cytokine - useful in vaccines to protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cochran MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09605291-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newcastle disease virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBDV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYTR ) SYNTRO CORP
                                                                                                                                                                                                                                                                                                                                                             protect against two or more c
is the product of the F gene
an antigen which can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant turkey herpes virus (rTH) which comprise a foreign DNA sequence encoding a cytokine inserted into a XhoI site within an
                                                                                   05-MAY-1997
                                                                                                            AAW10691;
                                                                                                                                       AAW10691 standard;
                                                                                                                                                                                                                                                                                                                                   Sequence
 poultry.
                                                        Newcastle disease virus fusion protein
                            Fowlpox virus; FPV; recombinant virus; vector; vaccine;
               immunisation;
                                                                                                                                                                                                           433
                                                                                                                                                                                                                                    4 TLSLKNDF-----KEIKTDELEIIIGGSGSLSTFFRLFNRSFTQALGK 46
                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1996-139689/14.
DB; AAT18203.
                                                                                                                                                                                                          and other avian viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDV;
                                                                                                                                                                                                                                                                 Similarity 33...
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease virus; infectious laryngotracheitis virus; IBV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDV; ILV
                                                                                                                                                                                                                                                                                                                                     553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 179-180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Junker DE,
                                                                                   (first
                 NDV;
                                                                                                                                                                                                                                                                                                                                     A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0362240
94US-0288065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US10245
               haemagglutinin; fusion protein; antigen;
                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                               or more of these avian viruses. This sequence he F gene of the Newcastle disease virus and in the used in the recombinant vaccines.
                                                                                   entry)
                                                                                                                                                                                                                                                                              24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Singer PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249pp;
                                                                                                                                                                                                                                                                  Score 55.5; D
Pred. No. 29;
7; Mismatches
                                                                                                                                          553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     foreign DNA encoding a against Marek's disease
                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                            Length 553;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                     Gaps
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RESULT
AAY21983
                                                                                                                                                                                                                                                                                                                                                                                   Вb
                                                                                                                                                                                                                                                                                                               δÃ
Matches 16;
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            fusion (F) protein (AAW10691) are expressed by novel recombinant fowlpox virus (FPV). The genes (see also AA748510) for HN and F be inserted into homology vector 443-88.8 (see also AA748511) at unique Sfil site, yielding homology vector 507-26.22 (see also AA748502-05), which can be used to insert the NDV HN and F genes into fowlpox virus. The recombinant virus is used to deliver the vaccine antigens to poultry.
                                     07-JUN-1995;
26-FEB-1993;
28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 109-110; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant fowlpox virus - contg. a foreign DNA inserted into the fowlpox virus genome, used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9640880-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newcastle disease virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cochran MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYTR ) SYNTRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-1996.
                                                                                                                                                                                                         07-SEP-1999
                                                                                                                                                                                                                           AAY21983;
                                                                                                                                                                                                                                              AAY21983 standard; Protein; 553
Cochran MD,
                                                                            07-JUN-1995;
                                                                                               20-JUL-1999
                                                                                                                   US5925358-A
                                                                                                                                     Fowlpox virus
                                                                                                                                                         Newcastle disease
                                                                                                                                                                 Fowlpox virus;
                                                                                                                                                                                                                                                                                           (SYTR ) SYNTRO CORP
                                                                                                                                                                                                                                                                                                                4 TLSLKNDF-----KEIKTDELEIIIGGSGSLSTFFRLFNRSFTQALGK 46
                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                     ID No: 14 of US5925358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997-087060/08.
DB; AAT48510.
                                                                                                                                                                                                                                                                                                                                                                                    553 AA;
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Junker
                                                                                                                                                                                                         (first entry)
Junker DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORP
                                     95US-0484575.
93US-0024156.
94WO-US02252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0484790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US11187
                                                                                                                                                                 FPV;
                                                                              95US-0484575
                                                                                                                                                          virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE,
                                                                                                                                                         recombinant; vaccine; immunisation; chicken; NDV; irus; NDV; Fowlpox; infectious Laryngotracheitis.
                                                                                                                                                                                                                                                                                                                                              24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Singer
                                                                                                                                                                                                                                                                                                                                   ; Score 55.5; D; Pred. No. 29; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA
                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                        Length 553;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
prodn. of
                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                the
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RESULT
AAB36039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a recombinant fowlpox virus (FPV) comprising a foreign DNA inserted into a region of the fowlpox virus genome corresponding to a 2.8 kb EcòRI fragment, capable of being expressed in a host cell. The virus is used as a vaccine for immunising chickens against
                          The present sequence is provided in a specification relating to a recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNZ can be expressed in host cells infected with FPV. The recombinant FPV may be used in vaccines to protect animals (especially chickens) again fowlpox and, depending on the source of the foreign DNA, other disease
                                                                                                                                                                                                                                                                                                                                                                                                                             US6136318~A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fowlpox virus; FPV; antiviral; antibacterial; vaccine; Newcastle's disease virus; NDV; Marek's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by NDV SfiI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36039 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newcastle disease virus (NDV), Fowlpox, and infectious Laryngotracheitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fowlpox viruses, useful as vaccines for immunization of
chickens/turkeys against Fowlpox and Newcastle disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-418249/35
                                                                                                                                                                                                                                                Cochran MD,
                                                                                                                                                                                                                                                                                                                         26-FEB-1993;
28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-2000
                                                                                                                                 Disclosure;
                                                                                                                                                                                                         N-PSDB; AAC67862.
                                                                                                                                                                                                                                                                            (JUNK/) JUNKER D E. (COCH/) COCHRAN M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Newcastle's disease virus.
                                                                                                                                                           inserted into specific non-essential region
                                                                                                                                                                          New recombinant fowlpox virus useful as vaccines contains foreign DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infectious laryngotracheitis
laryngotracheitis
              particularly Newcastle's disease, Marek's disease or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 tlrisgefdvtyqknisiqdsqviitgnldistelgnvnnsisnalnk 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TLSLKNDF-----KEIKTDELEIIIGGSGSLSTFFRLFNRSFTQALGK 46
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                                                                                                                                                                                                                     2000-686071/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Column 61-70; 108pp; English
                                                                                                                              Column 71-74; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                 Junker DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                       93US-0024156.
94WO-US02252.
                                                                                                                                                                                                                                                                                                                                                                  95US-0486414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment.
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Pred. No. 29;
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                                                                                                                                                             of the
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                                                                                                                                                           genome
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                            without the addition of exogenous proteolytic activity. Also it is possible to generate a stable transfected cell line that expresses the wild-type F protein in the virus envelope therefore providing infectious particles, useful in the form of a vaccine, especially against respiratory and/or gastrointestinal diseases. NDV can be easily cultured to very high titers in embryonated eggs. Mass culture of embryonated eggs is relatively cheap. NDV vaccines are relatively stable and can be simply administered by mass application methods e.g. drinking water or by spraying or by aerosol formation. The natural route of infection is by the respiratory and/or gastrointestinal tract which are also the major routes of infection of many other poultry pathogens. NDV can induce local immunity despite the presence of circulating maternal antibody. This sequence represents a protein encoded by the NDV strain LaSota genome which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                    This invention describes a novel avian paramyxovirus cDNA (I) which comprises a nucleic acid sequence corresponding to the 5' terminal end of the genome of avian paramyxovirus allowing the generation of end infectious copy of avian paramyxovirus. The cell line is useful for an infectious copy of avian paramyxovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Avian-paramyxovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newcastle disease virus LaSota
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peeters BPH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                            New avian paramyxovirus cDNA, useful
Newcastle disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     local immunity.
                                                                                                                                                                                                                                                                         the production of
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16; Conserv
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   AA;
                                                                                                                                                                                                                                                                        infectious
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastrointestinal disease; poultry pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection; lentogenic; F protein; vaccine;
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                                                                                                                                                                                                                                                                         lentogenic NDV (Newcastle Disease virus)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gielkens ALJ
                                                                                                                                                                                                                                                                                                                                                                                                                              for production of vaccine against
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Query Match
Best Local Similarity

24.4%;

Score 55.5; Pred. No. 29;

DB 21;

Length 553;

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RESULT
AAY58183
ID AAY5
The invention relates to a recombinant fowlpox virus (FFV)

CC comprising a foreign DNA inserted into a 4.2 kb EcoRI fragment

CC comprising a foreign DNA inserted into a 4.2 kb EcoRI fragment

CC comprising a foreign DNA inserted into a 4.2 kb EcoRI fragment

CC comprised in a host cell into which the fowlpox virus has been

CC introduced and encodes an antigenic protein. The antigenic protein

CC which may be expressed includes infectious laryngotracheits virus

CC (IITV) 91ycoprotein B (9B) or 91ycoprotein D(9D, ANY58184), Newcastle

CC disease virus (NDV) haemagglutinin (HN, ANY58182) or fusion (F) protein

CC disease virus (NDV) haemagglutinin (HN, ANY58182) or fusion (F) protein

CC disease virus on the same virus B or gD. The foreign DNA may

CC alternatively encode a cytokine such as chicken myelomonocytic growth

CC recombinant FPV is under the control of one or more synthetic pox

CC gene expression. The synthetic pox virus promoters that may be used are

CC gene expression. The synthetic pox virus promoters that may be used are

CC based on promoters of the vaccinia virus and include early promoter 1

CC (EPI), late promoter 1 (LPI), EP2 and LP2 (AAX9291-Z49294,

CC recombination between FPV DNA and a homology vector containing the

CC recombination are used as multivalent live vaccines for immunising fowl

CC against Marek's disease virus, NDV, LITVY and/or fowlpox virus. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Newcastle disease virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant fowlpox virus useful as a vaccine for immunizing against Marek's disease, Newcastle disease, Infectious Laryngotracheitis Virus and/or fowlpox -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Junker DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1993;
28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Columns 71-74; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYTR ) SYNTRO CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433
                  present sequence represents NDV fusion (F) protein
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)B; AAZ49295.
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94WO-US02252.
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501..527
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                                   C(II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. C(II), and (II) can have antibacterial activity and therefore can be used cin vaccination. The nucleic acids (I) may be used to produce the CC s. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the CC containing them which are used to produce hosts cells which express the CC containing them which are used to produce hosts cells which express the CC containing them which are used to produce hosts cells which express the CC containing them which are used to assay for other inhibitors of their cativity and therefore identify compounds that may be used for the CC containing the containin
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N-PSDB; AAH52982.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Page 386; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides from Staphylococcus epidermidis.useful for vaccinating against infections, e.g. endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLAX ) GLAXO GROUP LTD.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          open reading frame protein sequence SEQ ID NO:1358.
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Pred. No. 29;
7; Mismatches
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Query Match Best Local Similarity

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Score Pred. NO. ДВ 36;

22;

Length 583;

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ortein; 508 AA.  protein fragment SEQ ID NO: 55612.  protein fragm	:       syktgsykt 34	10; Mismatches 5; Indels 4; Gaps 1;
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16-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG44398;
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promoter;
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RESULT 15

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ID AAR35757

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AC AAR35757;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sweet; heat; resistance; protease.
                                                                                                                                                                                                                                                                                                                                                      30-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                            23-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monellin protein.
                                                                                                                                                               Sequence 96 AA;
                                                                                                                                                                                    Monellin, is a sweet protein, having high thermal resistance at low \mathsf{pH}'\mathsf{s} and also a high protease resistance.
                                                                                                                                                                                                                      Claim 1; Page 2; 29pp; Japanese.
                                                                                                                                                                                                                                          Single-stranded monellin protein - has high heat resistance in \ensuremath{\mathsf{cow}} pH range and high protease resistance
                                                                                                                                                                                                                                                                                 WPI; 1993-131302/16.
                                                                                                                                                                                                                                                                                                    (KIRI ) KIRIN BREWERY KK.
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                                                       1 MKKTLSLKNDFKEIKTDELEIIIGGSGSL 29
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42 mkktlyeenxfreikgyeyqlyvyasdkl 70
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Scoring table:

Minimum DB Maximum DB

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Title: Perfect score:

OM protein -

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Post-processing: Minimum Match 0% |
Maximum Match 100%
Listing first 45 summaries
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-663-566A-13
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,566A
FILING DATE: June 13, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEPHONE: (212)278-0400
                                                                Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                           TELEFAX: (212)391-0520
TELEX: 422523
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
TITLE OF INVENTION: and Uses Thereof
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1185 AVE
CITY: New York
STATE: New York
COUNTRY: USA
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7; Mismatches
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Sequence 332, App
Sequence 48, Appl
Sequence 48, Appl
Sequence 3, Appli
Sequence 11, Appl
Sequence 5, Appli
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Result No.

Score

553; <u>ن</u> Gaps

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; MOLECULE TYPE: protein US-08-484-575A-14
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/08023610 Patent No. 5928648
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Best Local Similarity 33.3%;
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TELEFAX: (212)391-0525
INFORMATION FOR SEQ ID NO: 14:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS: JOHN P. White
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mark D. Cochran and David E. TITLE OF INVENTION: Recombinant Fowlbox
                                                                                                                                                                                                                                                                                                   APPLICANT: Cochran Ph.D. Mark D
APPLICANT: Macdonald Ph.D., Richard D
TITLE OF INVENTION: Recombinant Herpesvirus
TITLE OF INVENTION: and Uses Thereof
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 TLRLSGEFDVTYQKNISIQDSQVIITGNLDISTELGNVNNSISNALNK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 553 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                    COUNTRY:
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FILING DATE:
                     APPLICATION NUMBER:
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30 Rockefeller Plaza
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 February 26, 1993
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Recombinant Fowlpox Viruses and Uses Thereof
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                     US/08/023,610
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                                                                                                                                                      ; TOPOLOGY: 11; MOLECULE TYPE: US-08-288-065A-13
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PATENT NO. 5901/01

PATENT NO. 5901/01

APPLICANT: Macdonald, Richard D

APPLICANT: Macdonald, Richard D

TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys

TITLE OF THE NOTION: HYT-050 and Uses Thereof
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Best Local Similarity 33.3%;
                                                                                      Query Match
Best Local Similarity
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TELEX: 422523
INFORMATION FOR SEQ ID NO:
                                                                       Matches
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CURRENT APPLICATION NUMBER: US/C
APPLICATION NUMBER: US/C
FILING DATE: Aug-09-94
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: line
VOLETT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
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LENGTH: 553 amino acid
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                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMULICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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433 TLRLSGEFDVTYQKNISIQDSQVIITGNLDISTELGNVNNSISNALNK 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                             TYPE: amino acid
                               4 TLSLKNDF-----KEIKTDELEIIIGGSGSLSTFFRLFNRSFTQALGK 46
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                                                                                                                                                                                                                               553 amino acids
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                                                                       Conservative
                                                                                                                                                                                                linear
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Pred. No. 3.4;
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Pred. No. 3.4;
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                                                                                                        DB 2; Length 553;
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US-08-477-459-14; Sequence 14, Application US/08477459; Patent No. 6001369
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; MOLECULE TYPE: protein
US-08-362-240A-13
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                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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NAME: White, John P
REGISTRATION NUMBER: 28,678

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)278-0400

TELEPAX: (212)391-0526
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TELEX: 422523
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk |
COMPUTER: IBM PC compatible
COMPUTER: IBM PC -DOS/MS-DOS
                                                                                                                                                                                                    APPLICANT: Mark D. Cochran TITLE OF INVENTION: Recombi TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
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APPLICANT: Junker, David
APPLICANT: Wild, Martha A
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                                                                                                                                                                                                                                                                                                                                                                         433 TLRLSGEFDVTYQKNISIQDSQVIITGNLDISTELGNVNNSISNALNK 480
                                                                   COUNTRY: USA
ZIP: 10036
                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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 COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                    ADDRESSEE:
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                              Floppy disk
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PC-DOS/MS-DOS
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                                                                                                                                                                                                                    Recombinant Fowlpox Viruses and Uses
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Pred. No. 3
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Patent No. 6123949
GENERAL INFORMATION:
                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 16; Conserv
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 Best Local Similarity
                                                                                                                                       TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/024,156
FILING DATE: 26-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                  MOLECULE TYPE:
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                                                                                                  TOPOLOGY:
                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                  LENGTH: 553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: John P. White
30 Rockefeller Plaza
                                                                                                                                                                                              : (212)977-9550
(212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cochran Ph.D, Mark D
VENTION: Recombinant
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                                                                                  protein
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 24.4%;
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Score 55.5;
Pred. No. 3.
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                 Length 553;
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RESULT 9
US-08-804-372A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 553
TYPE: PRT
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Best Local Similarity
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                                REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/08/486,414B
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cochran, Mark D.
APPLICANT: JUNKET, DAVIG E.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
FILE REFERENCE: 42771D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cochran, Mark D.
APPLICANT: Wild, Martha A.
APPLICANT: Winslow, Barbara J.
                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                 SEQUENCE CHARACTERISTICS:
                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          433 TLRLSGEFDVTYQKNISIQDSQVIITGNLDISTELGNVNNSISNALNK 480
                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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1185 Avenue of the Americas
553 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant Chimeric Viruses and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.4%; Score 55.5; D: 33.3%; Pred. No. 3.4;
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-804-372A-11
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PCT-US94-01826A-14
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                                                                                                                                                                                     RESULT 11
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                                                                                                                          Sequence 14, Application PC/TUS9402252A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                               APPLICANT: Syntro Corporation, et al. TITLE OF INVENTION: Recombinant Fowlp NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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STREET: New York
CITY: New York
CTATE: New York
TSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                     STREET:
                                    ADDRESSEE:
                                                                                                                                                                                                                                                                           4 TLSLKNDF-----KEIKTDELEIIIGGSGSLSTFFRLFNRSFTQALGK 46
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30 Rockefeller Plaza
                   E: John P. White
30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212)664-0525
                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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                                                                                           Recombinant Fowlpox Viruses and Uses Thereof
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Pred. No. 3.4;
7; Mismatches 20
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Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                    Mismatches
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COUNTRY:

New York

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RESULT 12
PCT-US95-10245-13
; Sequence 13, Application PC/TUS9510245
; GENERAL INFORMATION:
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PCT-US95-10245-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 14
                                                                          TELEX: 422523
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02252A
FILING DATE: 28-FEB-1994 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SYNTRO CORPORATION TITLE OF INVENTION: Recombinat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release, #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: John P. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 TLRLSGEFDVTYQKNISIQDSQVITTGNLDISTELGNVNNSISNALNK 480
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                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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nes 16; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
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                                TOPOLOGY:
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                                                                 LENGTH:
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           protein
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; ORGANISM: Arabidopsis thaliane US-09-564-805-228
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;Patent No. 5310678
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;T.;Millar, Neil S.
; TITLE OF INVENTION: NEWCASTLE
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                                                                                                                                                                                                                                                                                           FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Myriad Genetics, Inc
TITLE OF INVENTION: Chromosome
TITLE OF INVENTION: Gene and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/
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                                                                                                                                                                               LENGTH: 837
TYPE: PRT
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APPLICATION NUMBER: 885,765
FILING DATE: 15-JUL-1986
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473 LPNCLEKIRRDDMEIVILGTGSSQPSKYRNVSAIFIDLFSR 513
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                                                                             Local Similarity
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              7 LKNDFKEIKTDELEIIIGGSGS--
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Rommens, Johanna M
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Pred. No. 3
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Pred. No. 3
                                                                               score 55.5; D
pred. No. 5.8;
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RESULT 15

US-09-242-650A-6

Sequence 6, Application US/09242690A

Patent No. 6284534

GENERAL INFORMATION:

APPLICANT: WAINEA, YUTAKA

TITLE OF INFUNION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE

TITLE OF INFUNION: YEAST

FILLS REFERENCE: 049441/0118

CURRENT APPLICATION NUMBER: US/09/242,690A

CURRENT APPLICATION NUMBER: US/09/242,690A

CURRENT PILLNG DATE: 1999-02-23

PRIOR APPLICATION NUMBER: POT/JP97/02924

PRIOR FILING DATE: 1997-08-23

INUMBER OF SEQ ID NOS: 66

SEQ ID NOS: 6

CURRENT: PATENTIN Ver. 2.1

SEQ ID NOS: 6

US-09-242-690A-6

QUETY MATCH

Best Local Similarity 41.48; Fred. No. 0.59;

MAICHES 12; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

NAMECHES 12; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

US-09-242-690A-6

QY 1 MKKTISKNOFKEIKTDELEIIIGGSGSL 29

| III | III | III |
| Db 43 MKKTITEENGFREIKGYEYQLYVANSDKL 71

Search completed: July 30, 2002, 15:14:41
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length: 20000000000
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2: pir2:*
3: pir3:*
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     A;Gene: spr2036
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SULT 2 8126 8126 8126 8127 8128 8128 8129 8129 Species: Streptococcus pneumon Date: 22-Oct-2001 #sequence_re Accession: A98126 HOSKINS, J.A.; Alborn Jr., W.; R.; LeBlanc, D.J.; Lee, L.N.; P.; Sun, P.M.; Winkler, M.E. Bacteriol. 183, 5709-5717, 20; Authors: Yang, Y.; Young-Belli Title: Genome of the Bacterium Reference number: A97872; MUID Accession: A98126 Status: preliminary Molecule type: DNA Residues: 1-650 (XUR) Cross-references: GB:AE007317; Genetics: Genetics:	Query Match Best Local Similarity 33.3%; Pred. Matches 19; Conservative 10; Mis  Qy 2 KKTLSLKNDFKBIKTDELEIII	RESULT 1  F95260  ABC transporter permease protein C:Species: Streptococcus pneumonia C:Date: 03-Aug-2001 #sequence_revi C:Accession: F95260  R:Tettelin, H:; Nelson, K.E.; Paul on, J.D.; Umayam, L.A.; White, O:nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001  A:Authors: Loftus, B.J.; Yang, F. A; Title: Complete Genome Sequence A:Reference number: A95000; MUID:2 A;Accession: F95260  A;Status: preliminary A;Molecule type: DNA A;Residues: 1-850 <kur> A:Croos-references: GB:AE005672; PA:Experimental source: Strain TIGR C:Genetics: A;Gene: SP2231</kur>		30 54 23.8 226 1 32 54 23.8 226 1 32 54 23.8 226 1 32 54 23.8 243 2 10 54 24 23.8 24 24 24 24 24 24 24 24 24 24 24 24 24
O36 [imported] - Streptococcus pricon 22-Oct-2001 #text_change 22-Cinold, J.; Blaszczak, L.; Burgett, Lifkowitz, E.J.; Lu, J.; Matsushima M.; Zhao, G.; Zook, C.; Baltz, Freptococcus pneumoniae Strain R6.429245; PMID:11544234  DN:AAL00838.1; PID:g15459743; GSE	Score 69; DB 2; Length 850; Pred. No. 1.1; ; Mismatches 16; Indels 12; Gaps 2; DELEITIGGSGSLSTFERLFNRSFTQALGK 46 : :	probable SP2231 [imported] - Streptococcus pneumon de la comparison 03-Aug-2001 #text_change 03-Aug-2001	ALIGNMENTS	c49769 gap junction prote h33646 gap junction prote c96946 gap junction prote c96946 glutamine ABC tran f24727 hypothetical prote f64237 bNA-directed RNA p s16722 amino acid ABC tra b11537 amino acid ABC tra b111537 amino acid BC tra b11537 amino

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hypothetical protein YMR044w - yeast (Saccharomyces N;Alternate names: hypothetical protein YM9532.09 c;Species: Saccharomyces cerevisiae C;Date: 08-May-1995 #sequence_revision 01-Sep-1995 #;Accession: $52893 C;Accession: $52893 R;Odell, C.; Bowman, S.
                                                                                                                                                                                                                          submitted to the EMBL Data Library, A; Reference number: S52885 A; Accession: S52893
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A; Map position: 13R
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A; Residues: 1-475 <ODE>
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A;Gene: comC
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           RESULT
E89792
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A; Residues: 1-41 < KUR>
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                                                                                                            Conservative
                                                                                                                                                                                              GB:AE007317; PIDN:AAL00845.1;
  SA0272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.7%;
                                                                                                                        25.8%;
 [imported]
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Pred. No. 1.1;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NID:g695715; PIDN:CAA88410.1; PID:g695724; GSPDB:GN000:
                                                                                                           Score 58.5; DB Pred. No. 0.83; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 6.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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   Staphylococcus
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1.1;
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                                                                                                               14;
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                                                                                                                                                                                               PID:g15459751; GSPDB:GN00174
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      N315)
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A; Molecule type: 1 A; Residues: 1-398 A;Status: preliminary

<KUR>

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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: E89992
C;Accession: E89992
R;Kuroda, M; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Hiramafsu, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Wendt, U.K.; Hauschild, R.; Lange, C.; Pietersma, M.; Wenderoth, I.; von Schaewen, plant Mol. Biol. 40, 487-494, 1999
A;Title: Evidence for functional convergence of redox regulation in G6PDH isoforms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-0ct-2000 #sequence_revision 24-0ct-2000 #text_change 03-Nov-2000
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A;Residues: 1-1009 <KUR>
A;Cross-references: GB:BA000018; PID:g13700198; PIDN:BAB41496.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: acg9
C;Superfamily: glucose-6-phosphate dehydrogenase
C;Keywords: oxidoreductase
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                                                                     glycine betaine/1-proline transport ATP-binding protein proV BMEII0548 [imported C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: AC3578 [insert and insert and 
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A; Molecule type: mRNA
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A; Reference number: AD3252; A; Accession: AC3578
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity 34.1
12; Conservative
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Pred. No. 19
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C;Genetics:
A;Gene: uup
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: C97848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: D86806
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C:Species: Lactococcus lactis subsp. lactis
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D86806
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A; Residues: 1-593 < KUR>
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A; Residues: 1-408 <STO>
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Best Local S
Matches 17
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Best Local
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Best Local Similarity
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                  298
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                                                                                            Local Similarity hes 17; Conserv
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                                                     KKTLSLKNDFKEIKTDELEIIIGGSGS-LSTFFRLFNRSFTQALGK 46
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:AAL53790.1; PID:g17984720; GSPDB:GN00191
                                                                                            Score 56.5; pred. No. 29; 5; Mismatches
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                                                                                                                               DB 2;
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                                                                                              23;
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                                                                                                                             Length 593;
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F;223-339/Jomain: transmembrane
F;224-260/Jomain: transmembrane
F;302-318/Jomain: transmembrane
F;358-374/Jomain: transmembrane
F;358-374/Jomain: transmembrane
RESULT
E81339
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A;Map position: 12R
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                                                                                                            Ωy
                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z17475
A; Accession: T12258
                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Michalowski, C.B.; Quigley-Landreau, F.; Bohnert, H.J. submitted to the EMBL Data Library, May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pyrroline-5-carboxylate synthetase (EC 1.5.1.-) - common ice plant
C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;488-504/Domain: F;538-554/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z73264; NI
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-893 <BEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Benes, V.; Rechmann, S.; Nentwich, U.; Schwager, C.; Ansorge, W.; Voss, H. submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 06-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable membrane protein YLR092w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein L2528
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                                                                                                                                                                                                                                                   C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                    C; Superfamily: glutamate-5-semialdehyde dehydrogenase
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-719 < MIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T12258
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                                                                                                                                                                                                                                                                                        A;Gene: P5CS
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                                                                                                                                                                                                                                                                                                                             A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                   A;Status:
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Best Local S
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Best Local S
Matches 18
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                                                                                                              6 SLKNDFKEIKTDELEIIIGGSGSUST----FFRLFNRSF 40
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                                                                                                                                                                                                                                                                                                                                                                                 preliminary; translated
                                                                           SLCEQLKELNSDGYEVILVTSGAVSAGRQRLRFRKLVNSSF 77
                                                                                                                                                   l Similarity
15; Conserv
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                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56.5;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                     from GB/EMBL/DDBJ
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                                                                                                                                                 ed. No. 42;
Mismatches 13; Indels
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<TM7>
<TM8>
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Length 893; Indels

7;

Gaps

2

6;

Gaps

1;

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Q.W.; Quail, M.; Rajandream, M.A.; Rutherfo
Nature 403, 665-68, 2000
A; Title: The genome sequence of the food-bor
A; Reference number: AB1250; MUID:20150912
A; Accession: EB1339
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1250 <PAR>
A; Cross-references: GB:AL139076; GB:AL111166
A; Experimental source: serotype 02, strain N
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable NAD(P)-dependent oxidoreductase homolog lmo0546 [imported] - Listeria
C:Specles: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AC1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Authors: Kreft, J.; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1143
A;Status: preliminary
                                                                                                       probable NAD(P)-dependent oxidoreductase homolog lin0550 [imported] C;Species: Listeria innocua C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 **Change 27-Nov-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-416 <GLA>
A; Cross-references: GB: NC_003210; PIDN: CAC98625.1;
A; Cross-references: Strain EGD-e
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A; Authors: ok, C.; Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain C; Genetics: A; Gene: lmo0546
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                                                       D.; Jones, L.M.; Kars
Science 294, 849-852,
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Best Local Similarity
Matches 14; Conser
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Best Local Similarity
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   schlueter,
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                                                                                        Karst,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /modification enzyme Cj0690c [imported] - Campylobacter
   ; Kuhn, M.; .; Simoes, 1
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   Kunst, F.;
N.; Tierrez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55.
Pred. No.
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26;
      Kurapkat, G.; Madueno,
, A.; Vazquez-Boland, J
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Dussurget, O.;
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                                                                                                                          Baquero, F.; Berc
urget, O.; Entian,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F.; Berche, P.;
; Entian, K.D.;
                                                                                                                                                                                                               27-Nov-2001
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         Þ.;
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itian, K.I
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Voss, H.; V
            Maitournam,
Voss, H.; W
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Fsihi, H.
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Fsihi, H.
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Search Job tim

completed: ne: 389 sec

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2002,

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A; Fitle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AF1501
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Newcastle disease virus
C;Species: Newcastle disease virus
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988
C;Accession: A27008; F46329
R;Chambers, P; Millar, N.S.; Emmerson, P.T.
J, Gen. Virol. 67, 2685-2694, 1986
A;Title: Nucleotide sequence of the gene encoding the A;Reference number: A27008; MUID:87085486
A;Accession: A27008
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A; Residues: 1-416 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Newcastle disease virus evolution. A; Reference number: A46329; MUID:89204898 A; Accession: F46329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell fusion glycoprotein precursor - Newcastle disease virus N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
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                                                                                                                                                                               C;Superfamily: parainfluenza virus cell fusion protein C;Keywords: glycoprotein; membrane fusion; transmembrane protein E;1-25/Domain: signal sequence #status predicted <SIC> F;26-117/Product: cell fusion glycoprotein F2 #status predicted F;118-553/Product: cell fusion glycoprotein F1 #status predicted F;495-528/Domain: transmembrane #status predicted <TMN> F;85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M24697; NID:g293929; PIDN:AAA46648.1; A;Experimental source: strain BEA/45 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:X04719; NID:g60933; PIDN:CAA28426.1; A;Experimental source: strain Beaudette C R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K Virology 169, 273-282, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-553 < CHA>
                                Qy
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A; Residues: 1-553 <TOY>
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TLRLSGEFDATYQKNISIQDSQVIITGNLDISTELGNVNNSISNALNK 480
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                                                                                Score 55.5; I
Pred. No. 36;
7; Mismatches
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July 30, 2002, 15:14:49; Search time 15.86 Seconds (without alignments) 112.301 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5
Copyright (c) 1993 - 2000 Com
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              CB32_YEAST
HIS8_METJA
DNAA_RICCN
SYFB_PORPU
CXB2_MOUSE
CXB2_RAT
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CSP1_STRPN
SUL2_YEAST
P5CS_MESCR
CSP_STROR
VGLF_NDVB
             PROV_SALTY
LEU1_LACLA
YN48_YEAST
DNBI_HSV6U
DNBI_HSV6Z
GTRB_BPP22
GTRB_BPP22
                                                                VGLF_NDVQ
VGLF_NDVU
CYG2_HUMAN
PPNK_AQUAE
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p40969 saccharomyc
Q58365 methanococc
Q92h56 rickettsia
p51346 porphyra pu
Q00977 mus musculu
p21994 rattus norv
p45972 caenorhabdi
p47582 mycoplasma
Q9an14 edwardsiell
                                                                                                                                                                                                    Q04213 saccharomyc
Q54712 streptcoccc
Q12325 saccharomyc
O65361 m delta 1-p
O33689 streptcoccc
P06156 newcastle d
                                          P35936
P33615
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O67055
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3 newcastle d
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newcastle d
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human herpe
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methanococc
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ALIGNMENTS	Y830_METJA PSTH_ECOLI DNAA_MYCBO GTRB_ECOLI YP2A_STAAU UNG_MOUSE UNG_HUMAN DFRA_DIACA Y636_METJA Y061_MYCBC CG12_CANAL
	Q58240 P07655 P49916 P77293 P77293 P97931 P13051 P13051 P51104 Q58053 P473052 P473062 P473062
	methanococc escherichia mycobacteri escherichia staphylococ mus musculu homo sapien dianthus ca methanococc mycoplasma candida alb emericella

YMT4\_YEAST

STANDARD;

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RESULT 2
CSP1_STRPN
ID CSP1_S
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DT 15-DEC
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DT 16-OCT
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 55.4 kDa protein in MCM1-NUP116
YMR044W OR YM9532.09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
70 77

DOMAIN 186 195 F

DOMAIN 243 251

SEQUENCE 475 AA; 55426 MW;
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Odell C., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR000313; PWWP. Pfam; PF00855; PWWP; 1. SMART; SM00293; PWWP; 1.
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243
475 7
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38.9%;
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POLY-GLU.
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Pred. No. 2.8;
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CSP1\_STRPN STANDARD; PRT; 41 AA.
0544712;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Competence stimulating peptide type 1 precursor (CSP-1).

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Q12325;
15-JUL-1999
                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Sulfate permease 2 (High-affinity sulfate transporter
SUL2 OR SEL2 OR YLR092W OR L9449.1.
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du 2., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T., Hallsworth K., Hawkins J., Hiller L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.
                                                STRAIN=S288C / AB972;
Johnston M., Andrews S.,
                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                     YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                 SEQUENCE FROM N.A
                                                                                                               NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pheromone; Competence.
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Pfam; PF03047; ComC;
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EMBL; U76218; AAC44895.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic transformation in Streptococcus pneumoniae.", Proc. Natl. Acad. Sci. U.S.A. 92:11140-11144(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-RX / CP1200;
MEDLINE=96074663; F
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NCBI_TaxID=1313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Microbiol. 23:583-692(1997). FUNCTION: ACTS AS A PHEROMONE, FOR GENETIC TRANSFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE COMC FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 58.5; DI Pred. No. 0.34, 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1448B414E980E86A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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PSCS_MESCR STANDARD; PRT; 719 AA.

065361;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Delta 1-pyrroline-5-carboxylate synthetase (P5CS) [Includes: Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK); Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U53880; AAB67596.1; -.
EMBL; Z73264; CAA97653.1; -.
EMBL; Z73265; CAA97655.1; -.
EMBL; U53876; AAB67550.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular characterization of two in Saccharomyees Gerevisiae."; Genetics 145.627-635(1997).
-i- FUNCTION: HIGH AFFINITY UPTAKE
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    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: BELONGS TO THE SULFATE PERMEASE FAMILY.

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TE; PS01130;
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No. 19;
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Wohldman
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        CSP_STROR
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033689;
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Mendel; 29718; Mescr:1229;29718.

InterPro; IPR001048; Aaktnase.

InterPro; IPR002086; Aldehyde_dehydr.
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                                                            Competence
                                                                                   30-MAY-2000
30-MAY-2000
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     Streptococcus oralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Kinase
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CATALYTIC ACTIVITY: L-glutamate 5-semialdehyde + phosphate

NADP(+) = L-gamma-glutamyl 5-phosphate + NADPH.

ENZYME REGULATION: FEEDBACK REGULATED BY PROLINE.

PATHMAY: FIRST AND SECOND STEPS IN PROLINE BIOSYNTHESIS PATHMAY: FIRST BIOSYNTHESIS PATHMAY BIOSYNTHEST PATHMAY BIOSYNTHESIS PATHMAY BIOSYNTHESIS PATHMAY BIOSYNTHESIS
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SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GLUTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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IPR001057; Glut_5_kinase
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719 AA;
                                                      stimulating
                                                                          (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
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                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    719
77855 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293
                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.7%;
                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAMMA-GLUTAMYL PHOSPHATE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLUTAMATE 5-KINASE
                                                                                                                                                                                             PRT;
                                                         precursor (CSP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1510D11AF5559961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 719;
17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fusion 91-ycoprotein precursor [Contains: Fusi
                         "Newcastle disease virus evolution. II. La generating virulent and avirulent strains. Virology 169:273-282(1989).
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-87085486; PubMed=3025345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newcastle disease virus (strain Beaudette C/45) (NDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales,
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 179:6589-6594(1997).
-i- FUNCTION: ACTS AS A PHEROMONE, INDUCES CELLS FOR GENETIC TRANSFORMATION.
-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE COMC FAMILY.
                                                                                                                                 MEDLINE=89204898; Put
Toyoda T., Sakaguchi
                                                                                                                                                                                                                                                                                      Chambers P., Millar N.S., Emmerson Nucleotide sequence of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P06156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                             Nagai Y.
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     Newcastle disease virus."
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=11178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGLF_NDVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004288; ComC Pfam; PF03047; ComC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ000873; CAA04363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exchanges.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98012953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1303;
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                                                                                                                                                                                                                                        Gen. Virol.
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FUNCTION: THIS PROTEIN DIRECTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                        67:2685-2694(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                              PubMed=2705298;
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                                                                                                                                 Hirota H.,
                                                                                                                                                                                                                                                                                                                      Emmerson P.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55.5; DB Pred. No. 0.82; 5; Mismatches
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COMPETENCE STIMULATING PEPTIDE.
1276E5B6F72A1463 CRC64;
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FUSION OF VIRAL
                                                         II. Lack of
trains.";
                                                                                                                                    Gotoh B.,
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Best Local Similarity 33.3%;
Matches 16; Conservative
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P33613;
01-FEB-1994
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CARBOHYD
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DOMAIN
                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fusion glycoprotein precursor [Contains: Fusion fusion glycoprotein f1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDVH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000776; Fusion_gly.
Pfam; PF00523; fusion_gly; 1.
Glycoprotein; Fusion protein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Newcastle disease virus evolution. generating virulent and avirulent st Virology 169:273-282(1999).
-!- FUNCTION: THIS PROTEIN DIRECTS !
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                                                                                                                           SEQUENCE FROM N.A. MEDLINE-89204898; PubMed-2705298;
                                                                                                                                                                                         Paramyxoviridae;
NCBI_TaxID=11181;
                                                                                                                                                                                                                                    Newcastle disease virus (strain B1-Hitchner/47) (NDV). Viruses; ssRNA negative-strand viruses; Mononegavirales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                               Nagai Y.
                                                                                                         Toyoda
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SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES FUSION GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMILY.
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                                                                                                      T., Sakaguchi
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                                                                                                                                                                                                               Paramyxovirinae;
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                                                                                                         T., Hirota
                                         avirulent strains.
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Pred. No. 15;
7; Mismatches
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F1 PROTEIN.
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  FUSION OF VIRAL AND CELLULAR
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                                                                                                      Gotoh B., Kuma K., Miyata T.,
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Best Local
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                                                                                                                                                                     P33614;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fusion glycoprotein precursor [Contains: Fusi
Fusion glycoprotein F1].
                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000776; Fusion_gly.
Pfam; PF00523; fusion_gly; 1.
Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                               Virology 169:273-282(1989).
-!- FUNCTION: THIS PROTEIN DIRECTS FUSION OF
                                                                                                 SEQUENCE FROM N.A. MEDLINE=89204898; PubMed=2705298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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             -
                                                       generating virulent and avirulent
                                                                             Nagai Y.
                                                                                        Toyoda T., Sakaguchi T.,
                                                                                                                                    NCBI_TaxID=11184;
                                                                                                                                                Paramyxoviridae; Paramyxovirinae; Rubulavirus
                                                                                                                                                            Viruses; ssRNA negative-strand viruses;
                                                                                                                                                                                                                                                               VGLF_NDVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M24695; AAA46646.1; -.
                                                                  "Newcastle disease virus evolution.
                                                                                                                                                                                                                                                                                                                     433 TLRLSGEFDVTYQKNISIQDSQVIITGNLDISTELGNVNNSISNALNK 480
                                                                                                                                                                                                                                                                                                                                           4 TLSLKNDF----KEIKTDELEIIIGGSGSLSTFFRLFNRSFTQALGK
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SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-:
LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES FUSION GLYCOPROTEIN
                                                                                                                                                                                                                                                                                    8
SUBUNIT: THE MATURE FORM IS LINKED BY A DISULFIDE BOND.
                       MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D46329; D46329.
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                                                                                                                                                                                                                                                                                                                                                                l Similarity
16; Conserv
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                                                                                         Hirota
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CTTOPLASMIC. . .) (POT
N-LINKED (GLCNAC. . .) (POT
PALMITATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                Score 55.5; E
Pred. No. 15;
7; Mismatches
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F1 PROTEIN.
POTENTIAL.
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           DIMER
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                                                                  II. Lack of
                                                                                        Gotoh B.,
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            OF.
                                                                                                                                                            Mononegavirales;
                                                                                                                                                                                                        Fusion
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            POLYPEPTIDES F-1 AND
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                                  VIRAL AND CELLULAR
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                                                                                         Kuma K., Miyata T.,
                                                                  gene
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(POTENTIAL).
(POTENTIAL).
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                                                                   recombination
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RESULT

VOLF_NDVTG

ID

VOLF_NDVTG

P12571;

D7

O1-CCT-1989 (Rel. 12, Last sequence update)
D7

D1-CCT-1989 (Rel. 12, Last sequence update)
D7

D1-CCT-1989 (Rel. 140, Last annotation update)
D8

Fusion 91ycoprotein F1].

Fusion 91ycoprotein F1].

S8

Newcastle disease virus (strain Texas 9.b./48)
OC

Viruses; ssrNA negative-strand viruses; Monone
OC

Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX

NCBL_TaxID-11189;
RN

[1]

RP

SEQUENCE FROM NA.

RA

Schaper U.M., Fuller F.J., Ward M.D.W., Mehrot
RA

Schape
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CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2; Fusion glycoprotein F1]
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Pfam; PF00523; fusion_gly; 1.
Glycoprotein; Fusion protein; Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the state of the stat
                                                                                                                                                                                                                                                                                                                                                                                                   Schaper U.M., Fuller F.J., Ward M.D.W., Mehrotra Y., Stone H.O Stripp B.R., de Buysscher E.V., "Nucleotide sequence of the envelope protein genes of a highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newcastle disease virus (strain Texas g.b./48) (NDV). Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
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PIR; E46329; E46329.
         "Newcastle disease virus evolution. II. Lack of gene recombination
generating virulent and avirulent strains.";
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                                                                                                                                                                                                                                                                                                                  , neurotropic strain of Newcastle disease virus."; 165:291-295(1988).
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PALMITATE (POTENTIAL)
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F2 PROTEIN.
F1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55.5;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                               Gotoh B., Kuma K., Miyata T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions ong as its content is in
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) (POTENTIAL).
) (POTENTIAL).
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Query Match
Best Local Similarity
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-!- FUNCTION: THIS PROTEIN DIRECTS FUSION OF VIRAL AND CELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B29201; VGNZGB.
PIR; G46329; G46329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M23407; AAA46642.1; -. EMBL; M24698; AAA46649.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000776; Fusion_gly.
Pfam; PF00523; fusion_gly; 1.
                                                                                                              SEQUENCE
                                                                                                                                            LIPID
                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                         CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G46329; G46329.
P04849; 1SVF.
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553 AA;
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26
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                                                                                                                                                                                           116
553
136
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447
                                                                                                              59017 MW;
  24.4%;
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                                                                                                           N-LINKED (GLCNAC...) (POT
N-LINKED (CLCNAC...) (POT
PALMITATE (POTENTIAL).
PSF537269F876F9E9 CRC64;
  Score 55.5;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                               FUSION GLYCOPROTEIN F0. F2 PROTEIN. F1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR
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                                DB 1;
                             Length 553;
                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
                                                                                                                                                                   (POTENTIAL)
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СВ32
                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                 YEAST
"A zinc finger protein, essential for chron
constitutes a putative DNA binding subunit
cerevisiae kinetochore complex, Cbf3.";
                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes;
                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
                                                                               SEQUENCE FROM N.A. STRAIN=AC 502;
                                                                                                                                                                                   protein 3).
CBF3B OR CEP3 OR YMR168C OR YM8520.17C
                                                                                                                                                                                                                    Centromere DNA-binding protein complex CBF3 subunit B (Centromere
                                                                                                                                                                                                                                                                                  P40969
                                                                                                                                                                                                                                                                                                  CB32_YEAST
                                                              MEDLINE=95045413; PubMed=7957085;
                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                  STANDARD;
                essential for chromosome segregation, DNA binding subunit of the Saccharomyces
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                  803
                                                                                                                                                                                                                                   update)
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                                                                                                                                                          Saccharomycetes
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Matches

16;

Conservative

Mismatches

20;

Indels

Gaps

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                       HIS8_METJA
Q58365;
                                                                                                                                                                                                                         acetol-phosphate transaminase). HISC OR MJ0955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN~JAL-1 / DSM 2661 / ATCC 43
MEDLINE~96337999; PubMed~8688087;
                                                                                                                                                                                                                                                                               Probable histidinol-phosphate aminotransferase
                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 249705; CAABS
SGD; S0004778; CEP3
                                                                                                                                                                                              Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.
PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.
Nuclear protein; Chromosomal protein; DNA-binding; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00172; Zn_clus; SMART; SM00066; GAL4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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Strunnikov A.V., Kingsbury J., Koshland D.;
"CEP3 encodes a centromere protein of Saccharomyces cerevisiae.";
J. Cell Biol. 128:749-760(1995).
                                                        SEQUENCE FROM N.A
                                                                                                                                                                 Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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[2]
                                                                                                           NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metal-binding; Centromere.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001138; Zn2_CY6_fungal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 LQNDIKIIELKNDEMFSLIKGLGSLVPLNKLRQESLLE 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LKNDFK--EIKTDELEIIIGGSGSLSTFFRLFNRSFTQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: CBF3 IS FORMED OF FOUR SUBUNITS, CBF3A (CBF2), CBF3B (CEP3), CBF3C (CTF13) AND CBF3D.
SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: CONTAINS 1 zN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLUSTER DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONSERVED DNA SEQUENCE CALLED CDEIII, FOUND IN CENTROMERS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X81396; CAA57159.1; -. U12339; AAA57074.1; -. Z49705; CAA89804.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       608 AA; 71358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.2%;
                          / ATCC 43067;
                                                                                                                                                                      Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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; 2E24A0508080A09B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  373
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19;
                                                                                                                                                                      Methanococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 608
                                                                                                                                                                                                                                                                               (EC 2.6.1.9) (Imidazole
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Best Local Similarity
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                                                                                        Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histidine biosynthesis; Transferase; Aminotransferase; Pyridoxal phosphate; Complete proteome.
BINDING 231 231 PYRIDOXAL PHOSPHATE (PROBABLE).
SEQUENCE 373 AA; 42961 MW; 369DB5EB4C671218 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                         Chromosomal
                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (Rel. 41, 01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U67539; AAB98960.1; -. TIGR; MJ0955; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: PYRIDC
                                                                        "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                            MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                STRAIN-Malish
                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                      Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                      Rickettsia conorii
                                                                                                                                                                                                                                                                                           DNAA OR RC0916
                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                   DNAA_RICCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00599; AA_TRANSFER_CLASS_2; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001511; Aminotran_1.
InterPro; IPR001917; Aminotransf_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LKNDFKEIKTDELEIIIGGSGS---LSTFFRLF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES,
binds specifically double-stranded
                 of chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKELSKFLNVDEENIIVGGDGADEIIDTIFRTF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00155; aminotran_1
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                                                                                                                                                                                                                                                                                                         replication initiator protein
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                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
s an important role in the initiation and regulation replication. Binds to the origin of replication; it ally double-stranded DNA at a 9 bp consensus (dnaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.0%;
                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                    alpha subdivision; Rickettsiales;
eae; Rickettsia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   463 AA.
                                                                                                                                                                                                                                                                                                                            update)
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RESULT 13
SYFB_PORPU
ID SYFB_P
AC P51346
DT 01-0CT
DT 16-0CT
DT 16
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Mol. Biol. Rep. 13:333-335(1995).

- CATALYTIC ACTIVITY: ATP + L-phenylalanyl-tank(Phe) = diphosphate + L-phenylalanyl-tank(Phe).

- CSUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phenylalanyl-trna synthetase beta chain (EC 6
trna ligase beta chain) (Phers).
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                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00308; bac_dnaA; PROSITE; PS01008; DNAA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Rhodophyta;
                                                                                   EMBL; U38804;
                                                                                                                                        or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-AVONPORT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyra purpurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYFB_PORPU
                             Chloroplast
                                                        Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reith M.E., Munholland J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213
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by non-profit institutions as long as its content
ified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      box): 5'-TTATC(C/A)A(C/A)A-3'. DnaA binds to ATP and to acidic phospholipids (By similarity). SIMILARITY: BELONGS TO THE DNAA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Chloroplast
                                                                                                                                                                                                                                                                                                                                                                 CHAIN FAMILY. SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKTLSLKNDFKEIKT---DELEITIGGSGSLSTFFRLFN 37
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     720
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                                                                                         AAC08232.1;
     ΑĄ;
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     82592 MW; | 495E49947117F62A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.5;
Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1.1.20) (Phenylalanine--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                               Gap ju
                                                                                                                                                                                       PIR; C49769; C49769.
MGD; MGI:95720; Gjb2.
                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse embryonic development.
Dev. Biol. 146:117-130(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organization but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-92354576; PubMed-1322820;

Willecke K., Nicholson B.J., Dahl E., Kozjek G., Hennemann H.;

"Molecular cloning of mouse connexins26 and -32: similar genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gap junction be
GJB2 OR CXN-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q00977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CXB2_MOUSE
                                                                                                                                                                                                                               EMBL; M81445; AAA37495.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishi M., Kumar N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes
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                                                                                                        PROSITE;
                                                                                                                                                                                                               EMBL; M63803;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishi M., Kumar N.M., Gilula N.B.;
"Developmental regulation of gap junction gene expression
mouse embryonic development ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91285228; PubMed=2060697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495
                                                                                                                     PROSITE;
                                                                                                                                    SMART; SM00037,
                                                                                                                                                 PRINTS;
                                                                                                                                                            Pfam; PF00029; connexin;
                                                                                                                                                                           InterPro; IPR000500; Connexin.
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                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH MATERIALS OF LOW MM DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL. SUBGUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS. SUBGELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: LIVER, KIDNEY, INTESTINE, LUNG, SPLEEN, STOMACH, TESTIS, & BRAIN, BUT NOT HEART & ADULT SKELETAL MUSCLE. SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. BETA-TYPE (GROUP I)
                                                                                            junction;
                                                                                                                                                                                                                                                                                                                                                                  SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLKRN-KIIETTKLAIILGGSLDIRSEWSEPAHSLNWYEAKGIIENFFRKLNKS 547
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                                                                                                                                               PR00206;
                                                                                                        PS00407; CONNEXINS_1; PS00408; CONNEXINS_2;
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                                                                                            Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             distinct promoter sequences
                                                                                                                                                 CONNEXIN.
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25, Last sequence update
40, Last annotation updat
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31.5%;
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Pred. No. 26;
                                                  CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL)
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26) (Cx26).
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                                                                                                                                                                                                                                                                                                              restrictions
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                                                                                                                                                                                                                                                                                                                                      a collaboration
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TRANSMEM DOMAIN

POTENTIAL.
CYTOPLASMIC (POTENTIAL). EXTRACELLULAR (POTENTIAL)

POTENTIAL.

TRANSMEM

DOMAIN

DOMAIN

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Matches
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SEQUENCE
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gap junction beta-2 protein (Connexin 26) (Cx26).
GJB2 OR CXN-26.
                   TRANSMEM
DOMAIN
                                                                                                                                                                                                        PRINTS; PR00206; CONNEXIN.
SMART; SM00037; CNX; 1.
PROSITE; PS00407; CONNEXING
PROSITE; PS00408; CONNEXING
                                                                                                                                                                                                                                                                                                 PIR; A33646; A33646.
InterPro; IPR000500; Connexin.
Pfam; PF00029; connexin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Two homologous protein components of hepatic gap junctions."; Nature 329:732-734(1987).
-i- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1–18.
MEDLINE=88039049; PubMed=2823143;
Nicholson B.J., Dermietzel R., Teplow D., Traub O., Willecke K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                           Gap junction;
DOMAIN
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  TRANSMEM
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"Sequence and tissue distribution of a second protein of hepatic gap junctions, Cx26, as deduced from its cDNA.";
J. Cell Biol. 109:3391-3401(1989).
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                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 VK 168
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:||:|| |||| :: | ||| || || |||
                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH MATERIALS OF LOW MM DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL. SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS. SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: LIVER, KIDNEY, INTESTINE, LUNG, SPLEEN, STOMACH, TESTIS, & BRAIN, BUT NOT HEART & ADULT SKELETAL MUSCLE. SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. BETA-TYPE (GROUP I)
                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY
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21; Conserv
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MW;
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Pred. No. 8.5;
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CYTOPLASMIC (POTENTIAL).

H -> Y (IN REF. 2).

V -> I (IN REF. 2).

; 0D8178F7A339E0B6 CRC64;
                                                        POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                 POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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  POTENTIAL.
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Best Local S
Matches 21
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SEQUENCE
167 VK 168
                                       111 IKNEFKDIEEIKTQKVRI ----EGSLWWTYTTSIFFRVIFEAVFMYVFYIMYNGFFMQRL 166
                  45
                                                 7 LKNDFK---EIKTDELEIIIGGSGSL-----STFFR------
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                  46
                                                                                         Similarity
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226 AA;
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                                                                                         23.8%;
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Pred. No. 8.5;
6; Mismatches
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8.5;
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Search completed: July 30, 2002, Job time: 363 sec

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Result
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Copyright (c) 1993 - 2000 Compugen Ltd.
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O99q15 streptococc
O9apk6 streptococc
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O97n40 streptococc
O97n40 streptococc
O91651 lactococcus
O9cpe8 pasteurella
O33596 streptococc
O9cla3 saccharomyc
O9suk0 arabidopsis
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097330 plasmodium	_			4	7
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## ALIGNMENTS

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Qy 1 MKKTLSLKNDFKEIKTDELEIIIGGSGSLSTFFRLFNRSFTQALGK 46 	Query Match 100.0%; Score 227; DB 2; Length 46; Best Local Similarity 100.0%; Pred. No. 5.3e-22; Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps	FI CHAIN FROME, 1. 26 46 COMPETENCE STIMULATING PROTEIN. SQ SEQUENCE 46 AA; 5211 MW; 38FA62B6F78FC3BF CRC64;	Interpro; IPRO04	EMBL; AF277156;	EMBL; AF277155;	DR EMBL; AF277152; AAK01542.1;	J. Bacteriol. 18	Biofilms.";	"Natural Genetic Transformation of Streptococcus mutans	MEDLINE=21142515; PubMed=11208787;				OX NCBI TaxID=1309:		Streptococcus mutans.	GN COMC.	COMPETENCE STIMULATING PROTEIN P	01-DEC-2001 (TrEMBLrel. 19, Last annotation	01-JUN-2001 (TrEMBLrel, 17,		AC Q99015;	SULT 1

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PARENTAL DEPARTMENT OF SERVICE OF
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O9APK7;
O1-JUN-2001 (TrEMBLrel. 17, C
O1-JUN-2001 (TrEMBLrel. 17, L
O1-DEC-2001 (TrEMBLrel. 19, L
COMPETENCE STIMULATING PROTEI
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COMPETENCE STIMULATING PROTEIN.
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EMBL; AF277151; AAK01541.1; -. 

CHAIN. 26 46 COMPI
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EMBL; AF277154; AAK01544.1; -.

CHAIN 26 43 COMPE
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Li Y.H., Lau P.C.Y., Lee J.H., Ellen R.P., Cvitkovitch D.G.,
"Natural Genetic Transformation of Streptococcus mutans Grow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus mutans. Bacteria; Firmicutes;
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Li Y.H., Lau P.C.Y., Lee J.H., Ellen R.P., Cvitko
"Natural Genetic Transformation of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans.
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                                                                                                                                                                                   MKKTLSLKNDFKEIKTDELEIIIGGSGSLSTFFRLFNRSFTQA 43
                                                                                                           MKKTLSLKNDFKEIKTDELEIIIGGSGTLSTFFRLFNRSFTQA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKKTPSLKNDFKEIKTDELEIIIGGSGSLSTFFRLFNRSFTQALGK 46
                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 AA;
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5195 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.9%;
                                                                                                                                                                                                                                                                                              92.1%;
97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 220; DB Pred. No. 4.2e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPETENCE STIMULATING 38E0B9DB5B8FC3BF CRC64;
                                                                                                                                                                                                                                                                                              Score 209; DB 2
Pred. No. le-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPETENCE STIMULATING PROTEIN E5A78FC3BF6156C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46
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.2e-21
                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                  Length
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Q9L651
            REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9L651;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL LACTOCOCCIN 972 IMMUNITY PROTEIN (LACTIS PLASMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tettelin H., Nelson K.E., Paulsen J.T., Elsen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angluoll S., Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.", Science 293:498-506(2001).
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-IPLA 972; PLASMID=PBL1;
Sanchez C., Hernandez de Rojas A., Martinez B., Arguelles M.E.,
Suarez J.E., Rodríguez A., Mayo B.;
"Nucleotide sequence of pBL1, a bacteriocin-producing plasmid from
Lactococcus lactis IPLA 972.";
Lactococcus lactis IPLA 972.";
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SEQUENCE FROM N.A.
STRAIN=IPLA 972; PLASMID=PBL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9L651
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MEDLINE=21357209; PubMed=11463916;
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-IPLA 972; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      692 KKTFTTDNVFSFFNLGYTKEKKTFNINVSFPGNSQVSFESPTFYRLDTKTFTEAIQK 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKTLSLKNDF-----KEIKTDELEIIIGGSGSLS----TFFRLFNRSFTQALGK 46
                                                                                                                                                                                                                                                                                                                                  (MAR-2000)
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                                                                                                                                 (JAN-1998)
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                                                                                                                                 to the EMBL/GenBank/DDBJ databases
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Pred. No.
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Q9CPE8;
01-JUN-2001
01-JUN-2001
                            COMC
                                            O33596 PRELIMINARY; PRT; 48
033596;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
COMPETENCE STIMULATING PEPTIDE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROC OR PM0095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF242367; AAF64055.1; -- EMBL; AJ002203; CAC03468.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martinez B., Fernandez M., Rodriguez A., Suarez J.E.;
"Synthesis of lactococcin 972, a bacteriocin produced by Lactococcus
lactis IPLA 972, depends on the expression of a plasmid-encoded
bicistronic operon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL: AE006044; AAK02179.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasteurella multocida,
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martinez B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=IPLA 972; PLASMID=PBL1;
Streptococcus anginosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00521; P5CR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000304; P5CR. Pfam; PF01089; P5CR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-pec-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                       141 SLKPEYKOFTODLLNAVGKTCWVTQEADMHTITAGSGSSPAYFFLFMEAMQQAL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528
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                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      648 AA;
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29556 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                          26.28;
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17,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                Score 59.5; DI
Pred. No. 12;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                    -----ELEIIIGGSGSLSTFFRLFNRSFTQAL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63.5;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        011C7F11AD31A7D7 CRC64;
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                                                                                                                                                                                                                                  Lancet 357:1225-1240(2001).
EMBL; AP003130; BAB41496.1; -.
EMBL; AP003358; BAB56445.1; -.
Complete proteome; Hypothetical
SEQUENCE 1009 AA; 114781 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=NCTC 10713;
STRAIN=NCTC 10713;
MEDLINE-98012953; PubMed=9352904;
MEDLINE-98012953; PubMed=9352904;
Havarstein L.S., Hakenbeck R., Gaustad P.;
"Natural competence in the genus Streptococcus: Evidence that
"Natural competence in the genus Streptococcus: Evidence that
                                                                                                                                                                                                                                                                                                                                                                                                                         Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain Mu50). Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
$A0272 PROTEIN (HYPOTHETICAL PROTEIN SAV0283).
$A0272 OR SAV0283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q99WU3;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                          "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50); MEDLINE=21311952; PubMed=11418146;
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EMBL; AJ000864; CAA04341.1; -.
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NCBI_TaxID=158879, 158878;
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202 NDFPELFTDTLVNSISANKDITKWFQTYNKSLLSA 236
                                                                                                                                    Local
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                                                  9 NDFKEIKTDELEIIIGGSGSLSTFFRLFNRSFTQA 43
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                                                                                                                                    Similarity
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48
5621 MW;
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; 114781 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 58; DB
Pred. No. 2.8;
                                                                                                                                 Score 58; DB Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPETENCE STIMULATING PEPTIDE EB6DF7AEDE4E94DB CRC64;
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                                                                                                                                                                                                                                        protein.
16AD06D170CA31FE CRC64;
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                                                                                                                                                         Length 1009;
                                                                                                          Indels
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9SUKO;
Pfam; PF00479; G6PD; 1.
Pfam; PF02781; G6PD_C1.
PrINTS; PR00079; G6PDHDRGNASE.
PRODOM; PD001129; G6PD; 1.
PROSITE; PS00069; G6P_DEHYDROGENASE; 1.
PROSITE; PS00069; G6P_DEHYDROGENASE; 1.
Glucose metabolism; NADP; Oxidoreductase.
SEQUENCE 516 AA; 59171 MW; A7623780F053CA1C CRC64;
                                                                                                           EMBL; AJ010970; CAB52674.1; HSSP; P11411; 1DPG.
                                                                                                                                                                                                                                                                   MEDLINE-99364543; PubMed-10437832; MEDLINE-99364543; Lange C.,
                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49) (G6PD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          James A.B., Slaughter C., Meaden P.G.; "Characterization of partial coding sulfate transporter sequences from Saccharomyces pastorianus and Saccharomyces bayanus."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF364410; AAK32879.1; ".
InterPro; IPR001902; Sulfate_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULFATE TRANSPORTER SUL2-LA (FRAGMENT).
Saccharomyces pastorianus (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9C1A3;
O1-JUN-2001 (TrEMBLrel. 17,
O1-JUN-2001 (TrEMBLrel. 17,
O1-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                        DELTA-LACTONE 6-PHOSPHATE + NADPH
-!- PATHWAY: FIRST STEP IN PENTOSE PH
-!- SIMILARITY: BELONGS TO THE GLUCOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9C1A3
                                                                                                                                                                                                "Byidence for functional convergence of redox regulation isoforms of cyanobacteria and higher plants."; plant Mol. Biol. 40:487-494(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                  InterPro; IPR001282; G6PD.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTLSLKNDFKEIKTDELEIIIGGSGSLSTFFRL----FNRSFTQA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                           Schaewen A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISKSFGRVNDYKVVPDQEL-IAIGVSNLLGTFFNAYPATGSFSRSALKA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 AA; 49519 MW; 137117A0D12BD31F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                             Brassicales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.38;
                                                                                                                                                          IN PENTOSE PHOSPHATE PATHWAY.

TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                             Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57.
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                      Pietersma M., Wenderoth I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5;
38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453
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Best Local Similarity
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Best Local Similarity
                                    Q9AHY9
Q9AHY9;
Q1-JUN-2001 (TIEMBLrel. 17,
Q1-JUN-2001 (TIEMBLrel. 17,
Q1-DEC-2001 (TIEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCT-2000 (TrEMBLrel. 19, Last sanotation update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49) ((
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
                                                                                                                                                                                                                                                                                                           InterPro; IPRO01282; G6PD.
Pfam; PF00479; G6PD; 1.
Pfam; PF02781; G6PD; 1.
PRINTS; PR00079; G6PDHDRGNASE.
PRODOM; PD001129; G6PD; 1.
PROSITE; PS00069; G6P_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3.
Sequence features of the regions of 4,251,695 bp covered b
Photorhabdus luminescens (Xenorhabdus luminescens)
                          YFAA (FRAGMENT).
                                                                                                                                                                                                                                                                                   Glucose metabolism; NADP; Oxid
SEQUENCE 516 AA; 59157 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence features of the regions TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                       1 MKKTLSLKND--FKE----IKTDELEIII-GGSGSLS---TF---FRLFNRSF 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    æ
                                                                                                                                                                                                                                                                                                                                                                                                                            and BAC clones.";

Res. 7:217-221(2000).

CATALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE + NADP(+) = D-GLUCONO-DELTA-LACTONE 6-PHOSPHATE + NADPH.

PATHWAY: FIRST STEP IN PENTOSE PHOSPHATE PATHWAY.

SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKTLSLKND--FKE----IKTDELEIII-GGSGSLS---TF---FRLFNRSF 40
                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY
                                                                                                                                                              MEKRSTLKNDSFVKEYNPVTETGSLSIIVLGASGDLAKKKTFPALFNLFHQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEKRSTLKNDSFVKEYNPITETGSLSTIVLGASGDLAKKKTFPALFNLFHQGF
                                                                                                                                                                                                                                                                                                                                                                                          P11411;
                                                                                                                                                                                                                                                                                                                                                                                                          AP000381; BAB02125.1;
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41.5%;
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                                                                                                                                                                                                                                                                                                  Oxidoreductase
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                                                                                                                                                                                                                 Score 57.5; D
Pred. No. 44;
7; Mismatches
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EMBL/GenBank/DDBJ
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Pred. No. 44;
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DDBJ databases
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01-MAY-2000
01-MAY-2000
01-DEC-2001
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J. Bacteriol. 181:6238-6246(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-2125535; PubMed-11325940; Ciche T.A., Bintrim S.B., Horswill A.R., Ensign J.C.; Ciche T.A., Bintrim S.B., Horswill A.R., Ensign J.C.; "A phosphopantetheinyl Transferase Homolog Is Essential for Photorhabdus luminescens To Support Growth and Reproduction of Entomopathogenic Nematode Heterorhabditis bacteriophora."; J. Bacteriol. 18:3117-3126(2001).
                                                                                                                                                                                                                                                             SMART; SM00382; AAA;
SMART; SM00116; CBS;
                                                                                                                                                                                                                                                                                                      EMBL; AF139575; AAF04258.1; ...
InterPro; IPR00359; AAA.
InterPro; IPR003439; ABC_transp
InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR000644; CBS.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-NCDO 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00109; ketoacyl-synt; 1.

Pfam; PF02801; ketoacyl-synt_C; 1.

PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.

NON TER 591 591
                                                                                                                                                                                         PROSITE; PS00211; ABC_TRANSPORTER; ATP-binding; Transport.
SEQUENCE 407 AA; 45696 MW; D5DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000794; Ketoacyl-synt.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    - !- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P39435; 1KAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 QRVNRDRIGVILGGGGNGNTLFSLAGRQQTPYLRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 KEIKTDELEITIGGSGSLSTFFRLFNRSFTQALGK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 34.
                                                                         Local Similarity es 16; Conser
EIKTDELEIIIGGSGS-LSTEFRLENRSFTQALGK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.) (TrEMBLrel.
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                                                                                                                                                                                      45696 MW; D5DFBC0F8764B3A9 CRC64;
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                                                                                             24.9%;
                                                                                                                                                                                                                                                                                                                                                                             AAA.
ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13,
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma
                                                                    ; Score 56.5; DI
; Pred. No. 46;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Last annotation update)
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Q9KIF7
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Best Local
                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20318987; PubMed=10860977;
van der Heide T., Poolman B.;
van der Heide T., Poolman B.;
"Osmoregulated ABC-transport system of Lactococcus lactis stress via changes in the physical state of the membrane.
""" Natl. Acad. Sci. U.S.A. 97:7102-7106(2000).
                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
0PUAA (BETAINE ABC TRANSPORTER ATP BINDING PROTEIN).
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01-OCT-2000
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01-OCT-2000
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SMART; SM00116; CBS; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001687; ATP_GTP_A.
Interpro; IPR000644; CBS.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis.";
J. Mol. Microbiol. Biotechnol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bouvier J.,
Gutierrez C.
  MEDLINE=21235186; PubMed=11337471; Bolotin A., Wincker P., Mauger S.,
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InterPro; IPR003439; ABC_transportr.
                                                  STRAIN-IL1403
                                                                                                                                                                                                                                                                                  NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                           Lactococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
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wes 16; Conserv
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407 AA; 45
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irmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Last annotation update)
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Pred. No. 46;
3; Mismatches
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RESULT Q9RQ06

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Query Match Best Local :

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Search completed: July 30, 2002, 15:20:30 Job time: 376 sec
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RY "The complete genome sequence of the lactic acid bacterium Lactococcus
RY lactis sgp: lactis IL1403,",
RY Genome Res. 11:731-753(2001).
CC (ABC TRANSPORTERS)
CC (ABC TRANSPORTERS)
CC (ABC TRANSPORTERS)
CR EMBL; AF234619; AAF37878.1; -.
CR EMBL; AF234619; AAF37878.1; -.
CR EMBL; AF006375; AAK05550.1; -.
CR Interpro; IPR003593; AAA.
CR Interpro; IPR003593; AAA.
CR Interpro; IPR003439; ABC_transportr.
CR Interpro; IPR003439; ABC_transportr.
CR Interpro; IPR003439; ABC_transportr.
CR Interpro; IPR003439; ABC_transportr.
CR ROMODIS; ABC_tran; 1.
CR Pfam; PF00057; CBS; 2.
CR SMART; SM00312; AAA; 1.
CR SMART; SM00116; CBS; 2.
CR PROSITE: PS00211; ABC_TRANSPORTER; 1.
CR PROSITE: PS002211; PS002211; PS002211; PS002211; PS002211; PS002211; PS002211; PS00
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Best Local Similarity 45.7%; Pred. No. 46;
Matches 16; Conservative 3; Mismatches
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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       1446
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       AAY114065
AAY03650
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AAW899134
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AAY11170
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    AAG98391
AAW83369
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S. pneumoniae Orni
S. pneumoniae hist
Streptococcus pneu
Streptococcus pneu
S. pneumoniae deri
S. epidermidis ope
S. pneumoniae argB
S. pneumoniae ISSA
S. pneumoniae prot
Escherichia coli p
Streptococcus pneu
                                                                                                                                                                                                                                                                         Description
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rum	AAE00426	22	9		112	45
Plasmodium falcipa	AAB18236	21	1346		112.5	44
. burgdorferi	AAY20060	20	490		112.5	43
B. burgdorferi ant	AAY20061	20	471		112.5	42
Human DOCK180 prot	AAW03515	17	1865		113	41
Histidine kinase p	AAY28601	20	451		113.5	40
Streptococcus pneu	AAY81506	21	443		113.5	39
m	ABB47270	22	543		114	38
Staphylcoccus aure	AAY05736	20	457		114	37
	AAW86351	20	904		114.5	36
Drosophila melanog	ABB58194	22	1167		115	35
A. thermophilum th	AAW57445	19	850		115	34
Drosophila melanog	ABB69644	22	1079		115.5	33
B. burgdorferi ant	AAY19980	20	1494		116	32
	AAY19981	20	1477		116	31
O	AAB28685	21	618	٠	117	30
Nisin C of Lactoba	AAY06667	20	600		119	29
Nisin nisT gene pr	AAR95269	17	600		119	28
~	AAU03143	22	436		122	27
S. epidermidis ope	AAG81558	22	451		124	26
Novel human diagno	ABG29521	22	952		124.5	25
Plasmodium falcipa	AAY31946	20	4134		K >	24
	AAG82102	22	298		133	23
H. pylori HPS024 p	AAB46327	22	565		134	22
-	AAW71554	19	565		w	21
H. pylori GHPO 128	AAW98798	19	565		ω	20
Protein encoded by	AAU15085	22	1120		35.	19
	AAY95040	21	478		135.5	18
ichia col	ABB52567	22	606		w	17
taphylococcus	AAW75788	19	363		41.	16
taphylococcus	AAU37208	22	363		142.5	15
taphylococcus	AAU37397	22	909		143	14
taphylococcus au	AAW69977	19	861	6.6	4	3
Streptococcus pneu	AAY57684	21	442		145.5	12

## ALIGNMENTS

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S. pneumoniae Ornithine carbamoyltran	16-JUL-1999 (first entry)	AAY14065;	AAY14065 standard; Protein; 446 AA.	SULT 1

sferase

Ornithine carbamoyltransferase; argF/arcB family polypeptide; diagnosis; infection; therapy; immune response; otitis media; conjunctivitis; pneumonia; bacteraemia; sinusitis; pleural empyema; endocarditis; meningitis; matrix protein adhesion.

Streptococcus pneumoniae.

EP913476-A2

WPI; 1999-256630/22. N-PSDB; AAX57966. 30-OCT-1997; 06-MAY-1999. Brown JR, (SMIK ) SMITHKLINE BEECHAM CORP. 22-OCT-1998; Zalacain M; 97US-0961536. 98EP-0203571.

New Streptococcus pneumoniae ornithine carbamoy (argf/arcB) polypeptide and polynucleotide, us/

Page 2

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CC carbamoyltransferase protein (1) of the invention. The ornithine CC carbamoyltransferase protein is a (argf/arcB) family polypeptide. (1) CC carbamoyltransferase protein is a (argf/arcB) family polypeptide. (1) CC and polynucleotides (11) encoding it are useful for diagnosing diseases CC carbamoyltransferase gene by determining the nucleic acid sequence CC carbamoyltransferase gene by determining the nucleic acid sequence CC encoding (1), and/or analysing for the presence or amount of (1). They CC can diagnose the stage and type of infection. (1) is also useful for CC screening for compounds which affect activity of the protein by measuring CC the binding to (1) and observing the stimulation or inhibition of the CC enhance ornithine carbamoyltransferase activity, in addition to direct administration of ornithine carbamoyltransferase polypeptides to treat CC conditions associated with a lack of ornithine carbamoyltransferase polypeptides to treat CC polypeptide, or direct administration of antibodies against it induce an immune response to CC immunise and prevent disease. Anti-(1) antibodies induced by the CC polypeptide are also useful for isolating clones expressing (1), or for CC purifying the polypeptide by affinity chromatography. Diseases diagnosed, CC prevented or treated include otitis media, conjunctivitis, pneumonia, CC meningitis. (1), (1) and their (antipaonists can prevent admession of CC bacteria to matrix proteins, and are useful for use on wounds and body CC implants to prevent bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 27-28; 30pp; English.
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that shown in AAY14067.
                                                               the specification states that this sequence is identical to
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Sequence 446 AA;

Query Match Best Local

Similarity

34.6%; Score 752; DB 2 39.2%; Pred. No. 3e-58;

DB 20; Length 446;

Claim 6; Page 9; 37pp; English.

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ntnlnttcqnqvfrqvltv 442
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                                                                                                                                                       QNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILCDNAIEAAFESL 361
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Streptococcus pneumoniae. s. pneumoniae histidine kinase polypeptide 09-JUN-1999 17-JUN-1998 bacterial adhesion; wound. Histidine kinase; two component signal transduction system; TCSTS; bacterial; immune response; infection; otitis media; conjunctivitis; AAY03650 standard; Protein; 446 AA 20-JUN-1997; 20-JAN-1999. bacteremía; sinusitis; (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC. (first entry) 97US-0879941 98EP-0304782 pleural empyema; endocarditis; meningitis;

New Histidine Kinase polypeptide and polynucleotide - usef diagnostic reagents and for prevention and treatment of Streptococcus pneumoniae infections, especially meningitis 1999-083576/08 DB; AAX29247.

useful as

of the two component signal transduction system (TCSTS) in bacteria. The CC gene encoding the mature polypeptide can be isolated from S. pneumoniae CC 010093. Host cells containing a vector comprising the nucleic acid are CC 010093. Host cells containing a vector comprising the nucleic acid are CC underexpression of the protein of the protein. HK polypeptides and CC polynucleotides are useful for diagnosing diseases related to over or CC determining HK polypeptide or mRNA expression levels due to an infection of an organism with the HK gene. The polypeptides are also useful for CC screening for compounds which affect activity of the protein. These can CC enhance (agonist) HK activity. The polypeptides (administered directly, CC in a vector and as a vaccine) and antibodies induce an immune response to immuniae and prevent disease. Diseases diagnosed, prevented or treated CC include: bacterial infections, especially S. pneumoniae infections, which CC cause otitis media, conjunctivitis, bacteremia, sinusitis, pleural CC polypucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial infection. This represents a histidine kinase (HK) polypeptide which is a component

Sequence 446 AA;

B γΩ 밁 δõ Query Match
Best Local Similarity Matches 172; 66 plfgiglsflllrglpkkilifyglfpmilvelfyrgvsyfvlpflgggivdgdgnpifl 125 65 PLYFIALSTYLNRQNSLSLNIFYGLLPVASSDLFRRAIIFFILDGT-QGIV--MGSSIIT 121 12 LLTYLTVL--FLLELESKVSNVTLSKKELTLESISNELIMIAVT-----MVNVNLEYPAE 64 illyalvinglkiviffkvngigltfdrifkafllkfllgiifttfqflavskylsyfie 65 Conservative 34.6%; 86; Score 752; Pred. Mismatches No. 3e-58 DB 20; Length 446; 169; Indels 12; Gaps

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Streptococcus pneumoniae; response regulator; histidine kinase; infection; antibacterial; otitis media; conjunctivitis; pneumonia; bacteremia; sinusitis; pleural empyema; endocarditis; meningitis.
for diagnosing diseases, particularly for diagnosing the stage and type of an infection using PCR. Diseases related to expression or activity of RR proteins can be diagnosed by determining the nucleotide sequence encoding RR, or by analysing for the presence or amount of RR proteins. RR proteins can be used to screen for agonists and antagonists
                                                                                                                                                                                                                          New response regulator polypeptide and diagnostic reagents and for prevention Streptococcus pneumoniae infections
                                                                                           The present sequence represents histidine kinase from Streptococcus pneumoniae, which is cognate of the response regulator (RR) of the present invention. RR proteins and polynuclectides are useful as research reagents and as materials for discovery of treatments of,
                                                                                                                                                                                       Disclosure; Page 16; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                              Wallis NG;
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                                                       particularly for diagnosing the stage and type R. Diseases related to expression or activity of
                                                                                                                                                                                                                                              polynucleotide - useful as
and treatment of
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Best Local :
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                                                                                                     Streptococcus pneumoniae; response regulator; histidine kinase; infection; antibacterial; otitis media; conjunctivitis; pneumonia; beacterial; bleural empyema; endocarditis; meningitis.
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                        EP885963-A2
                                                              Streptococcus
                                                                                                                                                                                              Streptococcus pneumoniae histidine kinase.
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Pred. No. 3e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be diagnosed by determining the nucleotide sequence encoding RR, or by CC analysing for the presence or amount of RR protein. RR proteins can be used to screen for agonists and antagonists which interact with RR cC used to screen for agonists and antagonists which interact with RR proteins by observing the binding, or stimulation or inhibition of RR cC proteins by observing the binding, or stimulation or inhibition of RR cc activity, and RR proteins can be used in treatment to inhibit RR cC associated with a lack of RR protein. Diseases can be prevented by CC inoculating with RR protein, or a vector which expresses RR protein. RR cC proteins and polynucleotides can prevent adhesion of bacteria to matrix corporations, and can isolate or identify clones expressing RR proteins. CC infections, and can isolate or identify clones expressing RR proteins. CC and can purify the proteins by affinity chromatography. Diseases can disposed, prevented or treated include: otitis media; conjunctivitis; pneumoniae bacteremia; sinusitis; pleural empyema; endocarditis and consensations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents histidine kinase from Streptococcus pneumoniae, which is cognate of the response regulator (RR) of the present invention. RR proteins and polynucleotides are useful as research reagents and materials for discovery of treatments of and diagnostics for disease, and particularly for diagnosing the stage and type of an infection by PCR. Diseases related to expression or activity of RR can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New response regulator polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of Streptococcus pneumoniae infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 15; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wallis NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-037058/04
                                                                                                                                                          184 yeggiqsttvrhlilvfyllffmggikkldtylkeklqeelnqeqtlryrdmerysrhie
                                                                                                                                                                                                                                                                                             122 TYMIEFAGIALSYLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITMLLYYLLIQVLYVIE 181
                        302 QNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILCDNAIEAAFESL 361
                                                                  244 elykeirsfrhdytnlltslrlgieeedmeqikeiydsvlrdssqklqdnkydlgrlvni
                                                                                                                                                                                                                                              126 limifvcfivl--vflkwldydftrlrrefldtgfqksltkinwamgayylvmqslsyle
                                                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LLTYLTVL--FLLFLFSKVSNVTLSKKELTLFSISNFLIMIAVT-----MVNVNLFYPAE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                local Similarity
                                                                                                              SLYKDIRSFRHDYLNILTSLRIGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGHLANI
                                                                                                                                                                                                       SYNVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQIRNITQYSQQIE
                                                                                                                                                                                                                                                                                                                                      plfgiglsflllrglpkkilifyglfpmilvelfyrgvsyfvlpflgggivdgdgnpifl 125
                                                                                                                                                                                                                                                                                                                                                                                                                               illyalvinglkiviffkungigltfdrifkafllkfllgiifttfqflavskylsyfie 65
                                                                                                                                                                                                                                                                                                                                                                                     PLYFIALSIYLNRQNSLSLNIFYGLLPVASSDLFRRAIIFFILDGT-QGIV--MGSSIIT 121
172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0879528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.6%;
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Pred. No. 3e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 12;
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270 LASTEKTYHQILEKTGHQLQDTRYNIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVS 329

1 meqikeiydsvlrdssqklqdnkydlgrlvnirdralksllagkfikareknivfnvevp 60

Matches Query Match

Local Similarity

Conservative

40;

18.3%;

Score 398; DB 19; Pred. No. 2.1e-27; Mismatches

Length 175; Indels

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                                                                                                                                    This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see AAZ956173-Z96494) and their encoded proteins (see AAY85792-Y86182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of such a polypeptide. They can also be used to screen for compounds which interact with and inhibit or activate such a polypeptide. The polypeptides (or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in ammmal. The antagonists are particularly useful to identify antimicrobial compounds and antibiotics. They are also useful to determine their role in pathogenesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae proteins and related DNA - screening compounds for antibacterial activity % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) +\frac{1}{2}\left( \frac{1}{2}\right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-159452/14.
N-PSDB; AAZ96278.
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 404-405; 640pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. pneumoniae derived protein #120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 NPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIGLAKVNHILEHYP 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 rdralksllagkfikareknivfnvevpeeigvegmslldfltivsilcdnaievsaeas 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hodgson JE,
     175 AA;
                                                                                                       dysfunction and disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lonetto MA, Nicholas RO;
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    Query Match
Best Local S
Matches 107
                                                                                                                         ARH5008 represent oligonucleptide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                       (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucletc acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identity compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polypuclectide sequences from the present invention. AAH55091 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis SRl strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. epidermidis open reading frame protein sequence SEQ ID NO:780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG81843 standard; Protein; 432 AA.
                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis - \ensuremath{\mathsf{u}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAH52693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-2000; 2000WO-US30782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Page 240; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 diseifsfgasskgeergvglytvmkiveshpntnlnttcqnqvfrqvltv 171
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                      Local Similarity
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  Conservative 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                  17.4%;
                      Pred
                    Score 378.5; DB 2
Pred. No. 3.9e-25;
    Mismatches 181;
                                      DB 22;
    Indels
                                      432;
  63;
Gaps
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    12;
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7 ILSNGLLTYL----TVLFLLFLESKVSNVTLSKKELTLFSISNFLIMIAVTMVNVNLFY 61

Claim 12; Pages 311-312; 483pp; English

infections

Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial

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Вb
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 pneumoniae arga protein.

                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                      extracellular
                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW38531 standard; Protein; 108
                                                                                      WPI; 1998-008793/01.
N-PSDB; AAT98590.
                                                                                                                             Stodola
                                                                                                                                          Black MT,
                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                          14-MAY-1996;
                                                                                                                                                                                                                                    14-MAY-1997;
                                                                                                                                                                                                                                                             20-NOV-1997
                                                                                                                                                                                                                                                                                       WO9743303-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
                                                                                                                                                                                                                                                                                                                                                                               immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 TYMIEFAGIALS-----YLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITMLL--- 169
                                                                                                                                                                                                                                                                                                                                                                   cell immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 asqalvlvvimiii------ffy-----skvrwysivivlm-----stll 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enivpmkdklktrsikmngieklkvreikglittkiiqagekripisievpdeidrismn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAEPLYFIALSIYLNRQNSLSLNIFYGLLPVASSDLFRRAIIFFILDGTQGIVMGSSIIT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fstkgdnrglglstlkeltdsnenvlldtviengyfvq 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSTKGSNRGIGLAKVNHILEHYPKTSLQTSNHHHLFKQ 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tvelsriigiivdnaieasenleepliniafidneesvtfivmnkcsddipkihelfegg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QILEKTGHQLQDTRYNIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEME 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kyk---rklqeieayyeytlriesinnemrkfrhdyvnilttlsdyireddmpglrkyfn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QNEIMAQKEAQIRNITQYSQQIESLYKDIRSFRHDYLNILTSLRLGIENKDLASIEKIYH 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ryyiiisfvlaiafiyfyiisqtnlqesnslnfyaiifvsitvllslvilllsafalrem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -YYLLIQVL-----YVIESYNV--IPTLKFRKFVVIVYLILFLILISFLSQYTKQKV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              syltnfitvaislyteniihniyfynifhfsifiilslilahlfkhllirfrysylylsk 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLDFITILSILCDNAIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKEN 398
                                                                                                                              RK;
                                                                                                                                          Hodgson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                 pneumoniae protein; genetic immunisation; antagonist; response; inoculation; antibody production; inhibitor response; antimicrobial compound; bacterial adhesion;
                                                                                                                                                                                                                                                                                                                                                    matrix protein; protein-mediated cell invasion; wound;
                                                                                                                                                                                                                                                                                                               pneumoniae.
                                                                                                                                                                                                          96US-0017670.
                                                                                                                                                                                                                                    97WO-US07950.
                                                                                                                                          Knowles DJC,
                                                                                                                                           Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                 inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208
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RESULT
AAW38530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a Streptococcus pneumoniae protein that, based con homology with a Staphylococcus aureus protein, is an argB protein, cand is encoded by a DNA sequence of the invention. The DNA sequences were isolated from S. pneumoniae strain 010093 (NCIMB 40794). The CS treptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the cativity of the proteins. Antagonists can be used to treat diseases compounds which interact with and inhibit or activate the caused by S. pneumoniae proteins, through genetic immunisation. They can calso be used to induce an immunological response in a mammal by incleic acids in a vector adequate to produce antibody and/or T cell immune responses to identify antimicrobial compounds which are capable of compounds which are capable of compounds their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the implantation of compounes in infections of there invention compounes in infections initiated other than by the implantation of compounes in infections of the invasion of the invasion of compounes in infections of the invasion of the invasion of compounds which are capable of compounds which are capabl
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    pneumoniae

                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T cell immune extracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW38530 standard; Protein; 106 AA
Novel Streptococcus pneumoniae proteins and related {\tt DNA} - useful diagnosing anti-microbial agents for treatment of bacterial
                                                                       WPI; 1998-008793/01
N-PSDB; AAT98590.
                                                                                                                                           Black MT,
Stodola RK;
                                                                                                                                                                                                                                                                                                                                    14-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                       14-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337 MELLDFITILSILCDNAIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 fgasskgeergvglytvmkiveshpntnlnttcqnqvfrqvltv 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENYSTKGSNRGIGLAKVNHILEHYPKTSLQTSNHHHLFKQLLII 440
                                                                                                                                                                  Hodgson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae protein; genetic immunisation; antagonist; response; inoculation; antibody production; inhibitor; response; antimicrobial compound; bacterial adhesion; matrix protein; protein-mediated cell invasion; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSSAKACNP NCBI g1:695615 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae.
                                                                                                                                                                                                                                                                                       96US-0017670.
                                                                                                                                                                                                                                                                                                                                    97WO-US07950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%;
48.1%;
                                                                                                                                                                    Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 258; DB 19;
Pred. No. 2.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                       Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT
AAY11170
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Best Local
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                                                          Black MT, n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in a mammal by inoculation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or T cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The DNA sequences were isolated from Streptococcus pneumoniae strain 0100993 (NCIMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins or delivery
              WPI; 1997-503111/46
N-PSDB; AAX30770.
                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                            streptococcus
streptococcal
                                                                                                                                                                                                                                                                                                                                                                                            S. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a Streptococcus pneumoniae protein that, based on homology with a Lactobacillus protein, is a LSSAKACNP NCBI gl:695615 protein, and is encoded by a DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 311; 483pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections
                                                                                                                                                               22-AUG-1996;
02-APR-1996;
                                                                                                                                                                                                               01-APR-1997;
                                                                                                                                                                                                                                              09-OCT-1997.
                                                                                                                                                                                                                                                                              W09737026-A1
                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY11170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY11170 standard; Protein;
                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 YYLLIQVLYVIESYNVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQ 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 IRNITQYSQQIESLYKDIRSFRHDYLNILTS 260
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64 yrdmerysrhieelykeirsfrhdytnllts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 yylvmqslsyleyeqgiqsttvrhlilvfyllffmggikkldtylkeklqeelnqeqtlr 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106
                                                                             Hodgson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                            pneumoniae
                                                                                                                                                                                                                                                                                                                                          pneumoniae strain 0100993; vaccine; immune response; infection; pneumococcal.
                                                                                                                                                                                                                                                                                                                                                                                            protein SEQ ID NO:280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĀΑ;
                                                                                                                                                               96US-0025788.
96US-0014690.
                                                                                                                                                                                                               97WO-US05306
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                                                                               Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 192; DB Pred. No. 1.9e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                               Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX30724 to AAX30946 represent genomic DNA sequences isolated from Streptococcus pneumoniae strain 010993. These genomic DNA sequences encode the novel proteins given in AAX1114 to AAX11367. The proteins, isolated from Streptococcus pneumoniae, can be used in vaccines against streptococcal infections and in assays for identifying compounds that inhibit or activate the activity of the proteins. The antagonists can be used to treat an individual having need to inhibit a bacterial protein. Vectors expressing the proteins can be used to induce a
            The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences given in AAH81202 to AAH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism. (I) have antibacterial and antibiotic activities, and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                            Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                           WO200148209-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterial growth inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG98391 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protective immune response in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding pneumococcal polypeptide(s)
gene therapy. Expression of (I) in a microorganism inhibits proliferation
                                                                                                                                               proliferation,
                                                                                                                                                                                                                                                                              (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                            23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                          19-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 YYLLIQVLYVIESYNVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQ 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 IRNITQYSQQIESLYKDIRSFRHDYLNILTS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 yrdmerysrhieelykeirsfrhdytnlltt 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 yylvmqslsyleyeqgiqsttvrhlilvfyllffmggikkldtylkeklqeelnqeqtlr 63
                                                                                                                                                                                             2001-457376/49
DB; AAH81447.
                                                                                                                                           nucleic acids encoding proteins required for Escherichia coliferation, useful for screening for antimicrobial agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                            Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                            2000WO-US34419
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                                                                                                                                                                                                                                                                                                            99US-0173005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.7%; Score 189; DB 18; 40.7%; Pred. No. 3.5e-09;
                                                                                                          596pp; English.
                                                                                                                                                                                                                                            2yskind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product regulared for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. In addition to the the sequences complementary to sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAH81295 to AAH81487 and AAH81488 to AAH81491 proteins given in AAG98239 to AAG98431, and AAH81488 to AAH81491
                                                                                                                                                                     Streptococcus pneumoniae; histidine kinase; antibacterial; diagnosis; Streptococcal; Heliobacter pylori; infection; bacteriostatic; microbi bacteriocidal; ulcer; gastritis; stomach cancer; gene therapy.
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                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                    Streptococcus pneumoniae histidine kinase
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                                                                                                                                                                                                                                                                                                                                  AAW83369;
                                                                                                                                                                                                                                                                                                                                                                         AAW83369 standard; Protein; 442 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 ilfglepyeistlfeqrqamlqsikegvvavddrgev–-tlindaaqellnyrksqddek 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 IFYGLLPVASSDLF--RRAIIFFILDGTQGIVMGSSIITTYMIEFAGIALSYL------F 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pggeisvtlhyrhgwlhcevnddgpgiapdkidhifdkgvstkgsergvglalvkqqven\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIRSFRHDYLNILTSLRLGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGH-LANIQND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 AA;
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8.2e-05;
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                                                                                                                                                                       bacteriostatic; microbial;
er; gene therapy.
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26-MAY-1998;

98EP-0304138

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents histidine kinase (HK) isolated from Streptococcus pneumoniae. HK polynucleotides and polypeptides are useful for diagnosing susceptibility to diseases by detecting mutations or C for diagnosing susceptibility to diseases by detecting mutations or C polymorphisms in the HK gene or analysing for the presence or amount CC of HK polypeptide expressed in a patient sample. HK PCR probes are useful for diagnosing diseases (especially Streptococcal), and can C characterise the stage and the species or strain causing the infection. The HK probes can also determine the response of the infectious organism CC the HK probes can also determine the response are useful for screening CC for antagonists, agonists and polynucleotides are useful for screening CC HK agonists, agonists and drugs against infectious micro-organisms. CC HK agonists and antagonists are bacteriostatic and bacteriocidal compounds which can be used in treatment to enhance (agonist) or block cantagonist or antisense sequence) HK activity, therefore treating conicrobial (especially Streptococcal) diseases, ulcers and gastritis, and Stomach cancer caused by Heliobacter pylori. Epitopes of HK polypeptides and polynucleotides are useful immungens for producing anti-HK polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies for vaccines to prevent bacterial infections, and HK polynucleotides can be used in genetic immunisation (gene therapy) to prevent infections. HK polypeptides and polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 34-35; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Streptococcus pneumoniae Histidine kinase polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of Streptococcal and Heliobacter pylori infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-001392/01.
N-PSDB; AAV72649.
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316 dyallakerelqidnslthqqaylnpsv-----
                                                                                               256
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                                             KGILSAKILEAQ------NKKIAVNVEVSSKIQLPEMELLDFITILSILCDNAIEAAFES 360
                                                                                               nmrenigrykdrdqylgvalgivdelnhhvlqilslssvqelrddretidllqmtqnlvk 315
                                                                                                                                            N-----KD-----LASIEKIYHQILE----KTGHQLQDTRYNIGHLANIQNDAV 306
                                                                                                                                                                                            eignlkeginslyghlltviadlhekneailqlekmkveflrgashelktplaslkilie
                                                                                                                                                                                                                                              NITQYSQQIESLYKD--
                                                                                                                                                                                                                                                                                            qflpytllasflisllvayiyartivapileikrvtrr----mmdldsqvrlrvdskd 195
                                                                                                                                                                                                                                                                                                                                              VIESYNVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQIR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qkataiaqslegkd---rqsieqvldlysqtsdikgtvkge-----mte------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lftkifiytfs----ifsvlviclhlai-----yflfpstylshrqetig 46
                                                                                                                                                                                                                                                                                                                                                                                              ---dklevkdslpldtdrqttslfieerevktqdggtmilqflasmdlqkeaeqisl 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.7%; Score 145.5; DB 20; Length 442; 21.7%; Pred. No. 0.00019; tive 70; Mismatches 154; Indels 151;
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                                                                                                                                                                                                                                                 --- IRSFRHDYLNILTSLRLGIE 266
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47 qkataiaqslegkd---rqsieqvldlysqtsdikgtvkge-----mte-

87

83 LNIFYGLLPVASSDLFRRAIIFFILD-----GTQGIVMGSSIITTYMIEFAGIALSYLF 136

lfakifiytfs----ifsvlviclhlai-----yflfpstylshrqetig 46

24 LFSKVSNVTLSKKELTLFSISNFLIMIAVTMVNVNLFYPAEPLYFIALSIYL-NRQNSLS 82

Matches 104; Query Match

Conservative

70;

6

Local Similarity

6.7%; 21.7%;

Score 145.5; DB Pred. No. 0.00019

DB 21;

Indels 151; Length 442;

Gaps

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RESULT
AAY57684
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                                                   present invention are also useful for the identification of agents or drugs which are useful in preventing bacterial proliferation or kill bacterial cells e.g. potential antiblotics. The peptides and methods are also useful for providing important epidemiological tools. The peptide are especially useful for the prevention of any disease caused by a bacterium e.g. Staphylococcus aureus, Acinetobacter, Enterococcus faecalis, Escherichia coli, Pseudomonas aeruginosa all of which can cause blood polsoning among other ailments, Mycobacterium tuberculosis which causes tuberculosis, Shigella dysenteria which causes dysentery, and Neisseria gonorrhoeae which causes gonorrhoea. The peptides are also useful in the treatment of infections due to Streptococcus pneumoniae a bacterial species that causes blood polsoning, middle ear infections, pneumonia and meningitis in humans. The present sequence represents a energy historia in the present sequence represents a pneumonia and meningitis in humans. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes peptide antibiotics which inhibit the growth of pneumococci, ABC transporter and two-component signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibiotic; growth inhibition; bacterial autolysis; regulation; antibacterial; infection; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae sensor histidine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY57684 standard; Protein;
Sequence
                                                                                                                                                                                                                                                                                                                                transduction system proteins from Streptococcus pneumoniae. The peptides are useful (especially in the form of a pharmaceutical composition) for the treatment of a bacterial infection or inflammations. Methods from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid and peptides, useful as antibiotic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-062151/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novak R, Tuomanen EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 --pgglvrigeregel-fienscsseeqeklaqsfsdnasrkvkgsgmglfvvkslleh 416
                                      histidine kinase from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 128-130; 151pp;
  442 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
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                                                                The present sequence represents a Staphylococcus aureus Histidine kinase. The protein is related, by amino acid homology to the Escherichia coli KdpD histidine kinase protein. The protein can be used to treat an individual in need of histidine kinase, while the antagonist is used to inhibit histidine kinase. DNA encoding and expressing histidine kinase are is used in immunological compositions. The active agents are useful
                                                                                                                                                                                                                  New DNA encoding Staphylococcus aureus histidine kinase used to prevent, treat, diagnose and vaccinate against - e.g. respiratory tract infections and cardiac, gastrointestinal, CNS, eye, kidney, urinary tract, skin, bone and joint disorders
                 for preventing, treating, diagnosing and vaccinating against infections of the upper and lower respiratory tract, cardiac disorders, gastrointestinal disorders, CNS disorders eye disorders, kidney and
                                                                                                                                                                                                                                                                                                       WPI; 1998-458839/40.
N-PSDB; AAV43778.
                                                                                                                                                                                   Claim 14; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                         Wallis NG;
                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1997;
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     urinary tract disorders, skin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 nmrenigrykdrdgylgvalgivdelnhhvlqilslssvqelrddretidllqmtqnlvk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevention; treatment; diagnosis; vaccine.
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disorders, and bone and joint disorders
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21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
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                                                                                                                            WO200170955-A2
                                                                                                                                                     Staphylococcus aureus
                                                                                                                                                                                                                  Staphylococcus aureus cellular proliferation protein #1567.
                                                                                                                                                                                                                                                                                            AAU37397 standard; Protein;
                                                                                                     27-SEP-2001.
                                                                                                                                                                             antibiotic;
                                                                                                                                                                                          Antisense; prokaryotic cellular
                                                                                                                                                                                                                                             14-FEB-2002
                                                                                                                                                                                                                                                                     AAU37397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunological response
                                                                            21-MAR-2001;
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; 2000US-191078P.
; 2000US-206848P.
; 2000US-207727P.
; 2000US-242578P.
; 2000US-253625P.
                                                                                                                                                                             antibacterial;
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                                                                            2001WO-US09180.
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used for assaying genetic variation and raising response against e.g. Staphylococcus aureus.
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                                                                                                                                                                            drug
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Pred. No. 0.00081;
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Cc Note: The sequence data for this pattent did not form part compounds in the printed specification, but was obtained in electronic cf fra wino introm will be a compound to the printed specification at the sequence and the province in this pattent did not form wino introm wino introm
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3;
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16-FEB-2001;
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LCDNAIE---AAFESLNPEIQLAFFKKNGSIVFIIQN----
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 143; DB 22;
Pred. No. 0.00087;
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STKEKQIDVSKIFKENYST 401
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                                            The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery Cp programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
27-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck R, Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001WO-US09180
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Sequence
                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                             Example 3; Seq ID No 12801; 511pp; English.
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 363
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2000US-269308P.
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Title: Perfect score:

US-09-833-017-4 2173 1 MNEALMILSNGLLT

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

231628 seqs, 244|25594 residues

Run

OM protein - protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

Minimum DB Maximum DB

seg length: 0 seg length: 20000000000

Total number of hits satisfying chosen parameters:

231628

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\*

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/cgn2\_6/ptodata/2/iaa/FCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PcTUS\_COMB.pep:\*

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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
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US-08-874-138-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08874138 Patent No. 5882889
                                    Matches 172;
                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
APPLICANT: Wallis, Nicola
TITLE OF INVENTION: No. 5
                                                                                                                                                                                            NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
ZIP: 08
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CONTROL OPERATING SYSTEM:
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CITY: Lawrenceville
STATE: NJ
  FILING DATE:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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US-09-140-466-2

US-08-740-223A-22

US-08-714-070A-1

US-08-477-451-16

US-09-172-422-1

US-09-172-422-1

US-07-793-467-4

US-07-783-861C-2

US-08-740-223A-8

US-08-373-579-6

US-08-418-95-6

US-08-65-926-6

US-08-740-223A-6

US-09-351-457-4

US-09-351-500-4

US-09-561-500-4
                                   86;
                                  Score 752; DB 2; Length 446;
Pred. No. 8.9e-58;
86; Mismatches 169; Indels 12;
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Sequence 22, Appli
Sequence 12, Appli
Sequence 15, Appli
Sequence 16, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 4, Appli
                                    Gaps
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Result No.

Score

Match

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Description

Sequence

Sequence Sequence

Sequence

score greater and is derived

derived by analysis of the total score distribution.

SUMMARIES

US-08-874-138-6
US-09-147-116-2
US-09-747-116-2
US-09-148-207A-327
US-08-858-207A-327
US-08-858-207A-327
US-09-081-689-2
US-09-081-689-2
US-09-081-68-985-2
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US-08-981-98-2
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US-08-18-14-3
US-09-627-376-11
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US-09-084-346-2

Sequence Sequence

Sequence

145.5 141.5 117 117 114 113 113 112.5 112.5 108

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US-08-879-941-2
US-08-879-941-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 446 amino acid
                                                                                                                                                                       NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GMT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wallis, Nicola TITLE OF INVENTION: NOVEL
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 ELYKEIRSFRHDYTNLLTSLRLGIEEEDMEQIKEIYDSVLRDSSQKLQDNKYDLGRLVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 SLYKDIRSFRHDYLNILTSLRLGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGHLANI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 LIMIFVCFIVL--VFLKWLDYDFTRLRREFLDTGFQKSLTKINWAMGAYYLVMQSLSYLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 997 Lenox un
CITY: Lawrenceville
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                        TYPE:
                  TOPOLOGY:
                                     STRANDEDNESS:
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                                                                       446 amino acids
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997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                      609-520-3259
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wallis, Nicola TITLE OF INVENTION: NOVEL
                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 NTNLNTTCQNQVFRQVLTV 442
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TELEFAX: 609-520-3259
                                                                                                                                     FILING DATE
                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                         COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                     ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 997 Lenox D
CITY: Lawrenceville
                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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997 Lenox Drive, Building
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                                                                    362 NPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIGLAKVNHILEHYP 421
                                                                                                                                                                                                                                                                                              244 ELYKEIRSFRHDYTNLLTSLRLGIEEEDMEQIKEIYDSVLRDSSQKLQDNKYDLGRLVNI
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                                                                                                                                                 RDRALKSLLAGKFIKAREKNIVFNVEVPEEIQVEGMSLLDFLTIVSILCDNAIEVSAEAS
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Pred. No. 8.9e-58;
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TOPOLOGY: linear
US-09-747-116-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6348328
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                                                                                                                                                                                                                                                                                              APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Black, Michael APPLICANT: Hodgson, John APPLICANT: Knowles, David APPLICANT: Nicholas, Richard
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 SLYKDIRSFRHDYLNILTSLRLGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGHLANI 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 NPEIQLAFFKKNGSIVFIIONSTKEKQIDVSKIFKENYSTKGSNRGIGLAKVNHILEHYP 421
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                                                                OPERATING SYSTEM:
                                                                                                                                                       ZIP:
                                                                                                                                                                     COUNTRY:
APPLICATION NUMBER: US/08/858,207A
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US-08-858-207A-326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 326,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nicholas, ALLIANT APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-MAY-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                  APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM
                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 MELLDFITILSILCDNAIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 ENYSTKGSNRGIGLAKVNHILEHYPKTSLQTSNHHHLFKQLLII 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Gimmi, Edward REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                     STREET: 709 Swederand CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FGASSKGEERGVGLYTVMKIVESHPNTNLNTTCQNQVFRQVLTV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSLLDFLTIVSILCDNAIKASAEASQPHVSIAFLKNGAQETFIIENSIKEEGIDISEIFS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26, Application US/08858207A 6348328
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Knowles, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Black, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                           09-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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48.1%;
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                                    P50475
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                                                  US-09-081-689-2
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 442 amino acid
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SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,347
FILING DATE: 30-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Throup, John
APPLICANT: Biswas, Sanjoy
TITLE OF INVENTION: Histidine Kinase
NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dechert,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 YYLLIQVLYVIESYNVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQ 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 4000 CITY: Philadelphia
                                                                               LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP:
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Zalacain, Madgalenaa
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SYSTEM: Windows 95
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41.8%; Pred. No. 9.1e-10;
1tive 21; Mismatches 32; Indels
6.7%; Score 145.5;
                                                                                                                                                                                                                                                                                                                                                                                     US/09/081,689
                                                                                                                                                                                                                                                 36,795
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DB 4;
Length 442;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6071894
GENERAL INFORMATION:
                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/022,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
SEQUENCE CHARACTERISTICS:
                                                                                      NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                               FILING DATE: 25-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 60/039,478
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wallis, Nicola G. TITLE OF INVENTION: No. 6071894el Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256
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                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4000 Bell CITY: Philadelphia
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                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LFTKIFIYTFS-----IFSVLVICLHLAI-------YFLFPSTYLSHRQETIG 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19103-2793
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09046086
Patent No. 6127147
GENERAL INFORMATION:
APPLICAMT: Wallis, Nicola G.
TITLE OF INVENTION: No. 6127147e1 Compounds
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                    COMPUTER: IBM COMPATIBLE |
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,086
FILING DATE:
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 TIILMIFLIG------IILLSIWTRSFIIGFLAAIINVFVFNYFFTEPRYTFEVY 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         829 -GSNKYFKDNQKESMGLGLYLVQTIL-HKHQSNLQ 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402 KGSNR-----GIGLAKVNHILEHYPKTSLQ 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   777 LIENAVKHTSTDTKINLSIRYASY,EQ---IEFAVIDEGPGISLEEQQ----KIFEPFYT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 LCDNAIE--AAFESLNPEIQLAFFKKNGSIVFIIQN----STKEKQIDVSKIFKENYST 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     717 KLQSSNVQIKLQPYLVSELVEBIDMILERRHLKKRITVSSSVNLQFIHIDSKLILQALFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 NIQNDAVKGILSA------KILEAQNKKIAVNYEVSSKIQLPEMELLDFITILSI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               662 SHDIRTPLTTIMGNLDILVSHSKDMSIIEK--EQLLV---HSFQESQYLYLLVTNILSLT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 RHDYLNILTSLRLGIE-----NKDLASIEKIYHQILEKTGHQLQDTRY-----NIGHLA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 ILAIDYQSSQVINPYDASILESMLNELSLAVENVTLLKQTRESMLQAERQLTHSNFLRSI 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 -FLSQYTKQKVQN------EIMAQKEAQIRNITQYSQQIESLYKD------IRSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542 NQSKVIKTIPLQNHIDNTTQQHEQALSWVIKNERQAGATTDTFPGINKWLIPIGTSPIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513 QTYTVENLLINAGYQI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 REDYPITEI-VSILTSILTSALLKQIKEQYSITKKQLYRTDLLEQEND------SIK 512
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                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 TVLFLLFLFSKVSNVTLSKKELTLFSI--SNFLIMIAVTMVNVNLF-----YPAE-- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                     ZIP: 19103-2793
                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                         Philadelphia
                                                                                                                                                                                                                                                                      PΑ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NQLLQQSIT-----IYVI 541
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; STRANDEDNESS: sin
; TOPOLOGY: linear
US-09-046-085-2
                                                                                                                                                                                                                                                                          US-09-299-378-4
Sequence 4, Application US/09299378
Patent No. 6245545
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/299,378
CURRENT FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 618
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                                                                                                                                  APPLICANT: Higgins, Lauren S.
APPLICANT: Dalton, Michael A.
APPLICANT: Kong, Huimin
TITLE OF INVENTION: Method For Cloning And Producing The Swal Restriction
TITLE OF INVENTION: Endonuclease
FILE REFERENCE: Swal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/043,489 FILING DATE: 10-APR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 ATNLFILTMIICTIITYLLYNNYFVA-------MAVYYVVISLIMLDNFKKMK 153
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 NRL--NTLMFYIL-----LIIHYFIICYFVFSVHPMLSLFFFYSAFAVPF-TFKNNVKKT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 SDLFRRAIIFFILDGTQGIVMGSSIITTYMIEFAGIALSYLFLSVFNVDIGRLKDSLTKM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 KELTLESISNELIMI-AVTMVNVNLEYPAEPLYEIALSIYLNRQNSLSLNIFYGLLPVAS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 KDTSIAEISSILYLIFPIAGIFFNEVYGPKWLYIISVIVF-----SLS----YLILVIVN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MI - - - TRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESLNKVREIIDDVKLPSFIEEID -- SIRKVLKDADIDFTFE -- NKELAQVLSPTKQSMVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVKKRLIPMNITMLLYYLLIQVLYVIESYNVIPTLKFRKFVVIVYLILFLILISFLSQYT 214
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; TYPE: PRT ; ORGANISM: Staphylococcus warneri US-09-299-378-4
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US-08-963-901-2
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Best Local Similarity
Matches 116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08963901 Patent No. 6270992
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                     APPLICANT: Kosmatka, Anna L.
APPLICANT: Shilling, Lisa K.
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: NOVEL HISTIDINE KINASE
NUMBER OF SEQUENCES: 8
                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert P
                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 TKINILTMMYYLYNDISIFDKVKPNIYAIDFVYQEKHKEFNLFNYFNSQNQNFINDNFEN 210
                                                                                                                     STREET: 4000 Bell & CITY: Philadelphia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                  COUNTRY : US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 IPNTLLTKKKVLDPACGTGIFSIAFIHEIFNRQISKNSIVDF-INNYLVNIDVSNEMINF 150
OPERATING SYSTEM:
                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LSNGLLTYLTVL-----FILFLFSKVSNVTLSKKELTLFSISNFLI------MIAV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KINDSLHEELLKKGIKNKKRIGLGNLEVFKNPKLFIRQSANKLIATFDGKMSASNNSLYI 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDIVIGNPPYVS--LYGRRAINKSEDKRQFLIRNYDFIPKNVKNGKFNYTMFFIENGLQL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEGKQPQIKLSDLK---TIPLCFNEEINSKLL----IFAENATKKNNELESSLEKINQII 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIGLAKVNHIL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILCDNAIEAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIRSFRHDYL---NILTSLRLGIENKDLASIEKIY-----HQILEKTGHQLQDTRYNIGH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQIRNITQYSQQIES------LYK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKEAIVSIKDWQNNNTIQINQDIWLHDKFYRFNISDKKINSILEKVYNKSDELQYYFPKK 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKMKV-----KKRLIPMNITMLL----YYLLI---QVLYVIES-YNVIPTLK--FRKF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKKNGTLTFIVDITLLESSFESIRKYILETAIIKQLDINLKAFSDVVSGQIIISLLKNAS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TMVN------VNLFYPAEP-LYFI-----ALSIYLNRQNSLSLN----
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                                                                                19103
                                                                                                                                                            E: Dechert Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.4%; Score 117; DB 4; Length 618; ilarity 21.4%; Pred. No. 0.038; Conservative 76; Mismatches 187; Indels 164;
                                                                                                                                                                                                                                                                                                                           Traini, Christopher M.
                                                                                                                                                                                                                                                                                                                                             Walllis, Nichola G.
                   IBM Compatible
  DOS
                                                                                                                                                            1717 Arch Stre
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                                                                                                       US-08-588-985-2
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                                                                                                                             RESULT
Sequence 2, Application US/08588985
Patent No. 5777994
PATENT INFORMATION:
APPLICANT: Michiyuki MATSUDA et al.
TITLE OF INVENTION: CDNA OF DOCK180 GENE AND DOCK180 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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APPLICATION NUMBER: US/08/963,901
FILING DATE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
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NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 F--ILDGTQGIVMGSSIITTYMIEFAGIALSYLFLSVFNVDIGR-LKDSLTKMKVKKRLI 161
                                                                                                                                                                                      434 GTIQFTQSNEY 444
                                                                                                                                                                                                                                421 PKTSLQTSNHH 431
                                                                                                                                                                                                                                                                                                                366
                                                                                                                                                                                                                                                                                                                                                         326 EQFAADEKSLII------LADLESINFLGNQRLLHQALSNLLINAIK--YTDVGGAI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 N---ILTSLRIGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGHLANIQNDAVKGILSA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 IGTLQYHFNKMRESLGQVDQMRQHFVQNVSHEIKTPLTHIHHLLSELQQTSDKTLRQQYI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 PMNITMLLYYLLIQVLYVIESYNVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 HLGQMNYQIMTVDQKGHKTFYG-EPFREDTLSQNAINNYLNNKDYHGIKDKPFALFVTGF 127
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                                                                                                                                                                                                                                                                                                QLAFFKKNGSIVFIIQN--STKEKQIDVSKIFKENY--STKGSNRGIGLAKVNHILE-HY 420
                                                                                                                                                                                                                                                                                                                                                                                               KILEAQNKKIAVNVEVSSKIQLPEMELLDFI-----TILSILCDNAIEAAFESLNPEI 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAIYSITVILESALISEVLTNVYYHYNLKASNDAKIMKTLKEARQYEQSAKPTHIQQYEK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I------MAQKEAQIRNITQYSQQ------IESLYKDI-----RSFRHDYL 255
                                                                                                                                                                                                                                                                          DIALQHSHNNIIFTISNDGSPISPQAE-ARLFERFYKVSKHDNSNGLGLAITKSIIELHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NDIYTITTQLSGLTTELLLLSELDNHQ------HLLFDDKIQVDQL------IKDIIRH 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96;
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

383 STKEKQIDVSKIFKENYSTKGSNRGIGLAKVNHILEHYPKTSLQTSNHHHLFK 435

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; ORIGINAL SOURCE:
US-08-588-985-2
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MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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LENGTH: 1865 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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1123 MFENEI---ITKL----DHEVEGGRGDEQYKVLFDKILLEHCRKHKYLAKTGETFVKLVV 1175
                                                                                                                                                                      1003 YADMLNKKFLDQANFELQLWNNYFHLAVAFLTQESLQLENFSSAKRAKILNKYGDMRRQI 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE
                                                                                                                                                                                                                                                                                                                                             886 HILEVLYRKDVGPTQRHV-QIIMEKLLRTVNRTVISMGRDSELIGNFVACMTAILRQMED 944
                                                                                                                                                                                                                                                                                                                                                                                                                                831 GLLTIQKLYCLIEIVHSDLFTQHDCREIL-----LPMMTDQLKYHLERQEDLEACCQLLS 885
                                       334 LPEMELLDFITILSILCDNAIEAA† ----FESLNPEIQL-----AFFKKNGSIVFIIQN 382
                                                                                                                          285 GHQLQDTRYNIG-HLANIQNDAVKĢILSAKIL-EAQNKKIAVNV-----EVSSKIQ 333
                                                                                                                                                                                                                                                                                                 183 YNVIPTLK-FRKEVVIVYLILFLILISFLSQYTKQ-----KVQNEIMAQKEAQIRNITQ 235
                                                                                                                                                                                                                                                                                                                                                                                     134 YLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITML------LYYLLIQVLYVIES 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 LLQLFRSINDMMSSMSDQTV-RVKGAALKYLPTIVNDVKLVFDPKELSKMFTEFILNVPM 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 NSLSLNIFYGLLPVASSDLFRRALIFFILDGTQGIVMGSSIITTYM-----IEFAGIALS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 LLELESKVSNVTLSKKELTLESISNELIMIAVTMVN-VNLEYPAEPLYETALSIYLN-RQ 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 805 Fift
CITY: Washington
STATE: D.C.
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                                                                                  GFEIRDMWYNLGQHKIKFIPEMVGPILEMTLIPETELRKATIPIFFDMMQCEFHSTRSFQ 1122
                                                                                                                                                                                                                                                         YHYAHLIKTFGKMRTDVVDFLMETFIMFKNLIGKNVYPFDWVIMN--MVQNKVFLRAINQ 1002
                                                                                                                                                                                                              YSQQIESLYKDIRSFR----HDYLNI----LTSLRLGIENKDLASIEKI---YHQILEKT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1865 amino acids
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IBM Compatible
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N: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
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US-08-971-988-2
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                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1865 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1176 RLMERLLDYRTIMHD-----ENKENRMSCTVNVLNFYKEIEREEMYIRYLYK 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Michiyuki MATSUDA et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
183 YNVIPTLK-FRKFVVIVYLILFLILISELSQYTKQ------KVQNEIMAQKEAQIRNITQ 235
                                                        886 HILEVLYRKDVGPTQRHV-QIIMEKLLRTVNRTVISMGRDSELIGNFVACMTAILRQMED 944
                                                                                            134 YLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITML---
                                                                                                                                                                                                         772 LLQLFRSINDMMSSMSDQTV-RVKGAALKYLPTIVNDVKLVFDPKELSKMFTEFILNVPM 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                           21 LLFLFSKVSNVTLSKKELTLFSISNFLIMIAVTMVN-VNLFYPAEPLYFIALSIYLN-RQ 78
                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                GLLTIQKLYCLIEIVHSDLFTQHDCREIL-----LPMMTDQLKYHLERQEDLEACCQLLS
                                                                                                                                                                   NSLSLNIFYGLLPVASSDLFRRAIIFFILDGTQGTVMGSSIITTYM-----IEFAGIALS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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                                                                                                                                                                                                                                                                                                                                                                                          spleen cell of homo sapiens
                                                                                                                                                                                                                                                                                               5.2%;
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                                                                                                                                                                                                                                                                           90; Mismatches
                                                                                                                                                                                                                                                                                               Score 113; DB Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                 DB 1; Length 1865;
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                                                                                                                                                                                                                                                                                 208; Indels
                                                                                          ---LYYLLIQVLYVIES 182
                                                                                                                                                                                                                                                                                 8O;
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; HYPOTHETICAL:
; ANTI-SENSE: N
US-08-462-949-2
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                                                       Matches
                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rasmussen
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1063
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1176 RLMERLLDYRTIMHD-----ENKENRMSCTVNVLNFYKEIEREEMYIRYLYK 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1003 YADMLNKKFLDQANFELQLWNNYFHLAVAFLTQESLQLENFSSAKRAKILNKYGDMRRQI 1062
                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 LPEMELLDFITILSILCONAIEAA-----FESLNPEIQL-----AFFKKNGSIVFIIQN 382
                 129 GIALSYLFLSVFNVD------IGRLKDSLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             945 YHYAHLIKTFGKMRTDVVDFLMETFIMFKNLIGKNVYPFDWVIMN--MVQNKVFLRAINQ 1002
                                                       Local Similarity
                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Robinson, Joseph R. REGISTRATION NUMBER: 33,448 REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFENEI ---ITKL----DHEVEGGRGDEQYKVLFDKILLEHCRKHKYLAKTGETFVKLVV 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFEIRDMWYNLGQHKIKFIPEMVGPILEMTLIPETELRKATIPIFFDMMQCEFHSTRSFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSQQIESLYKDIRSFR----HDYLNI----LTSLRLGIENKDLASIEKI----YHQILEKT
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805 Third Avenue
                                                                                                                                                                                                                                                                                                                                       201-753-6237
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                                                         Conservative
                                                                                                                                                                     NO
                                                                                                                                                                                                                           linear
                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                       single
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Component Signal Transducing Regulatory System from
Bactoroides Fragilis
                                                                       5.2%;
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                                                         64;
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                                                     Score 112.5; DB Pred. No. 0.073; 4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.25
                                                                                         DB 1;
-KMKVKKRLIPMNITM 167
                                                                                         Length 519;
                                                         Indels
                                                         71;
                                                         Gaps
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                                                                                                                                   US-08-023-764B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08023764B Patent No. 5679540
                                       Matches
                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rasmus
                                                                                                                                                                                                                                                                           TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (201)831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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   129 GIALSYLFLSVFNVD---
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CITY: Wayne
STATE: New J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 MSMFDROKATLKMKELD--ANELISGVINTFALKVERYNGKITSNLEATNPVIFADEMHI 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          462 FDKFYRVHTGNLHDVKGFGLGLAYVKKIIQDHKGT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 TN---VIFNLMDNAVKYK----KPEEDLVLDVYTWNEPGKLMISIODNGIGIKKENLKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 FKENYSTKGSNR-----GIGLAKVNHILEHYPKT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 KTGHQLQDTRYNIGHLANIQNDAVKGILS--AKILEAQNKKIAVNVEVSSK-IQLPEMEL 339
                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                           NAME: Barnhard, Elizabeth M
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States ZIP: 07470-8426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----YIFDSVSFMIPSMIF-TFVLLITFIFTIYIVFRQKKLTEMKNDFINNMTH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIELLYHF-SVIDKDGREVYRCSDYEEGGSEDSYTQPLFQNDPPAKMSIVKVHFPGKKD-
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                                       1 Similarity
73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Jersey
                                                                                                                                                                                                                                                               519 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rasmussen, Beth Ann
TENTION: Cloning and Identification of a Two
TENTION: Component Signal Transducing Regulatory System from
TENTION: Bacteroides Fragilis
                                       Conservative
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                                                                                                                                                                 .. protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1993
                                                                                                                                                                                                                           single
                                     5.2%; Score 112.5; DB
21.8%; Pred. No. 0.073;
tive 64; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                               31,658-00
   --IGRLKDSLT--
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                                                                         DB 1;
                                         127;
     -KMKVKKRLIPMNITM 167
                                         Indels
                                                                       Length 519;
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Gaps

250

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В
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US-09-081-686-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                   INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
                                                                                                                                       NAME: Falk, Stephen T
RECISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GMI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,339
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 TN---VIFNLMDNAVKYK----KPEEDLVLDVYTWNEPGKLMISIQDNGIGIKKENLKKV 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 LDFITILSILCDNAIEAAFESLNPEIQLAF----FKKNGSIVFIIQ-NSTKEKQIDVSKI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 MSMFDRQKATLKMKELD--ANELISGVINTFALKVERYNGKITSNLEATNPVIFADEMHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 -----YIFDSVSFMIPSMIF-TFVLLITFIFTIYIVFRQKKLTEMKNDFINNMTH 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 KTGHQLQDTRYNIGHLANIQNDAVKGILS--AKILEAQNKKIAVNVEVSSK-IQLPEMEL 339
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                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19103-2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 4000 Bell (CITY: Philadelphia
                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
    STRANDEDNESS:
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Shilling, Lisa K.
Wang, Min
Jaworski, Deborah D.
Ingraham, Karen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Dechert, Price & Rhoads
4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                      215-994-2222
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VENTION: Histidine Kinase
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single
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Ъ QУ В B ; TOPOLOGY: US-09-081-686-2 DЬ δÃ QΥ Ъ Qy Db Qy B δÃ DЬ Qγ Matches 96; Query Match 400 ---STKGSNRGIGLAKVNHILEHYP-----268 201 196 401 QIVTDKDESSGLGLYIVSNILESYQMDYRYLPYEHGMEFKISLQT 445 354 ISNAIK ---350 CDNAIEAAFESLNPEIQLAFFKKNGSIVFIIQN---STKE----KQIDVSKIFKENY--321 LAHSIGVTIENQLTDATRVVMSLRALD-----261 NIGDYKDHPKYIAKSINKIDQMSHLLEEVLESSKFQEWTECRETLTVKPVLVDILSRYQE 320 236 YSQQIESLYKD-----141 LLLYLPYTFLVTIAFSFVFSYFYTKRLLNPLFYISEVTSKMQDLDDNIRFDESRKDEVGE 200 139 VFNVDI--GRLKDSLTKMKVKKRLIPMNI-TMLLYYLLIQVLYVIESYNVIPTLKFRKFV 195 63 Local Similarity 94 VHDLDIKDGKLSNYIV------MLDMSVSTADGKQVTVQFVHGVDVY------KEAKNI 140 36 KELTLESISNELIMIAVTMVNVNLEYPAEPLYFIALSIYLNRQNSLSLNIFYGLLPVASS 95 96 DLFRRAIIFFILDGTQGIVMGSSIITTYMIEFAGIALSY---LFLS-------6 KLLTNSFLRSFAILGGVGLVIHIAIYLTFPFYYIQLE---GEKFNESARVFTEYLKTKTS 62 VIVYL-ILFLILISF---LSQYTKQKVQNEI------MAQKEAQIR------NITQ 235 D-----EIPSLLQSYSKSLTISAHLKRDIVDKRLPL 93 TRYNIG-HLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSIL 349 ------KDLASIEKIYH---QILEKTGHQ---VGKQINGMYEHLLKVIHELESRNEQIVKLQNQKVSFVRGASHELKTPLASLRIILENMQH 260 5.0%; Score 108; DB 4; Length 446; ilarity 18.3%; Pred. No. 0.15; Conservative 78; Mismatches 133; Indels 218; linear ----YSDKNGRVIISEQDGYLSIKNTCAPLSDQELEHLFDIFYHS -----KTSLQT 427 ....LQD ---KVLTNL Gaps 400 399 290 23;

408

Search completed: July 30, 2002, 15:14:44
Job time: 520 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: July 30, 2002, 15:15:18; Search time 29.21 Seconds (without alignments) 1450.715 Million cell updates/sec

Title:
Perfect score:
Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 20000000001

Post-processing: Minimum Match 0% | Maximum Match 100% | Listing first 45 summaries

Database : PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	Ф.	ū	4	ω.	2			Result No.
143	143	145.5	145.5	146	148.5	150.5	151	151	151	151.5	154	155.5	163.5	171.5	174	184.5	223.5	348	362	372	379	416	418.5	423.5	427.5	455	749	755		Score
6.6	6.6						٠		6.9	7.0	7.1	7.2	7.5	7.9	8.0	8.5	10.3	16.0	16.7	17.1	17.4	19.1	19.3	19.5	19.7	20.9	34.5	34.7		Query
885	538	442	442	1447	473	543	543	543	543	921	533	440	657	532	542	433	452	448	428	371	423	431	431	441	441	447	446	446		Length
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sensor protein Kdp	two-component sens	vncS, histidine ki	sensor histidine k	hypothetical prote	sensory transducti	two-component sens	probable 2-compone	two-component sens	hypothetical 60.6	alkaline phosphata	two-component sens	virS protein - Clo	probable integral	two-component sens	two-component sens	two-component sens	membrane associate	probable histidine	Ľ.	accessory gene reg	agrC protein - Sta	sensor histidine k	sensor histidine k	histidine protein	probable sensor hi	histidine kinase-l	sensor histidine k	histidine kinase (	*	Description

two-component sens	н83993	N	532	6.0	129.5	5
sensory transduct	C96927	Ν	339	6.0	129.5	44
hypothetical prot	G90127	N	590	6.0	130	43
hypothetical prot	C90100	N	714	6.0	130.5	42
methyl-accepting	F71975	N	564	6.0	131	41
probable sensor	D82180	N	538	6.1	133.5	40
methyl-accepting	G64532	N	565	6.2	134	39
sensor kinase Dpin	AD0579	2	553	6.2	134.5	38
hypothetical prote	B70113	N	569	6.2	135.5	37
hypothetical prot	E90604	N	542	6.2	135.5	36
hypothetical pro	G70124	2	754	6.3	136	35
hypothetical prote	C89940	2	733	6.3	136	34
acriflavin resista	F71727	N	1008	6.3	136.5	33
kinB protein - Bac	S32935	2	428	6.3	137	32
hypothetical prote	в89907	2	363	6.4	138.5	31
glycosyl transfera	A86783	N	824	б. 5	142	30

## ALIGNMENTS

A; Accession: H9/929 A; Status: preliminary A; Molecule type: DNA A; Residues: 1446 < KUR> A; Cross-references: GB: AE007317; PIDN: AAK99268.1; PID: g15458033; GSPDB: GN00174 C; Genetics: A; Gene: hk13 A; Gene: hk13 C; Keywords: phosphotransferase	Y, P.; Sun, P.M.; WINKLET, M.E.  J. Bacteriol. 183, 5709-5717, 2001  A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S. A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  A; Reference number: A97872; MUID:21429245; PMID:11544234	RESULT 1  H97929  h1stidine kinase (EC 2.7.3) [imported] - Streptococcus pneumoniae (strain R6)  C; Species: Streptococcus pneumoniae  C; Spate: 22-oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001  C; Accession: H97929  R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.  e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.
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2	IGLAK 4	353 AIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIGLAK 412	Ωу
4	ILCDN 354	295 YDLGRLYNIRDRALKSLLAGKFIKAREKNIVFNVEVPEEIQVEGMSLLDFLTIVSI	Db
Ñ	ILCDN 352	293 YNIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILCDN	Qy
4	LQDNK 294	235 MERYSRHIEELYKEIRSFRHDYTNLLTSLRLGIEEEDMEQIKEIYDSVLRDSSQKLQDNK	Db
Ñ	LQDTR 292	233 TTQYSQQIESLYKDIRSFRHDYLNILTSLRLGIENKDLASIEKTYHQILEKTGHQLQDTR	Qy
4.	LRYRD 234	175 VMQSLSYLEYEQGIQSTTVRHLILVFYLLFFMGGIKKLDTYLKEKLQEELNQEQTLRYRD	Db
2	AQIRN 232	173 LIQVLYVIESYNVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQIRN	Qy
4	3AYYL 174	117 DGDGNPIFLLIMIFYCFIYLVFLKWLDYDFTRLRREFLDTGFQKSLTKINWAMGAYYL	DЬ
Ñ	LYYL 172	115MGSSITTYMIEFAGIALSYLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITMLLYYL	Qy
Ġ	30GIV 1:	57 SKYLSYFIEPLFGIGLSFLLLRGLPKKILIFYGLFPMILVELFYRGVSYFVLPFLGQGIV 116	Db
4	-QGIV 114	56 NVNLEYPAEPLYFIALSIYLNRQNSLSLNIFYGLLPVASSDLFRRAIIFFILDGT-QGIV	Qγ
	FLAV 5	1 MNIAWILLYALVINGLEIVIFFKVDGIGLTFDRIFKAFLLKELLGIIFTTFQFLAV 56	Db
	MV 5	1 MNEALMILSNGLLTYLTVLFLLFLFSKVSNVTLSKKELTLFSISNFLIMIAVTWV 55	. Ao
	i; Gaps	les 175; Conservative 88; Mismatches 171; Indels 14;	Matci
		Query Match 34.7%; Score 755; DB 2; Length 446;	Quer

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Sensor histidine kinase BlpH, probable (imported] - Streptococcus pneumoniae (strain TIC C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: D95061
C;Accession: D95061
R;Tettelin, H:, Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heicon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
F96909
histidine kinase-like ATPase [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
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A;Residues: 1-446 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK74685.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0527
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A;Accession: D95061
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                           TRYNIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGQVYDGYSFTGLCIIIFNFFISLAFLKWLDYDFTSLRKEILDKAFQKSLTQINWIMGGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNIAWILLYTLVTNGL-----EIVIFFKVDGIDLTFERIFKAFLLKILLAFVFVMIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNEALMIL----SNGLLTYLTVLFLLFLFSKVSNVTLS-----KKELTLFSISNFLIMIA 51
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                                                                                                                                                                                               YTVMKIVESHPNTSLNTTCQNQVFRQVLTV 442
                                                                                                                                                                                                                                                                                                DNATEASVEASQPHVSTAFLKNGAQETFITENSIKEEGIDISEIFSFGASSKGEERGVGL
                                                                                                                                                                                                                                                                                                                                             DNAIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIGL 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNITQYSQQIESLYKDIRSFRHDYLNILTSLRLGIENKDLASIEKIYHQILEKTGHQLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLVMESLSFFEYEQSIQSKTVRHLILVFYLLFFMGVIKKLDTYLKEKLYERLEQEQALRY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGIVMGSSIITTYMIEFAGIALSYLFLSVENVDIGRLKDSLTKMKVKKRLIPMNITMLLY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDMERYSRHIEELYKEVRSFRHDYTNLLTSLRLGIEEEDMEQIKEVYGSVLKDSSQKLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 749; DB 2;
Pred. No. 2.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:g14972002; GSPDB:GN00164; TIGR:SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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C;Accession: F96909
R;Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; l
R;Nolling, J.; Breton, G.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F96909
A;Status: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-447 < KUR>
A; Cross-references: GB: AEO01437; PIDN: AAK78065.1;
A; Experimental source: Clostridium acetobutylicum C; Genetics:
A; Gene: CAC0080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                          409
                                                                                                                                                                                                                                                                                                                                                168
                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
405 GLSNLKDIIGKYPNVMLDTVIEDNQFKQIIDIK 437
                                                                                                                  349 LCDNAIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGI 408
                                                                                                                                                                                                                  289
                                                                                                                                                                                                                                                            225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 GLLTYLTVLFLLELESKVSNVTLSKKELTLESISNFLIMIAVTMVNVNLEYPAEPLYFIA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSIYLNRQNS---LSLNIFYGLLPVASS------DLFRRAIIFFILDGTQGIVMGSSII- 120
                                       GLAKVNHILEHYPKTSLQTSNHHHLFKQLLIIK 441
                                                                                      LLDNAIEASEKCDRPSMKVAVINKDKSVMIVIINNYNEEIPPIYKIYKRGFSTKGDNRGI
                                                                                                                                                                                                                                                         EFQSLQEYTNKLEKLHKDMRGFRHDYINILLSMAGYIQNRDLEGLERFFDDKIMPLSKAM
                                                                                                                                                                                                                                                                                                                                                FYNTNVVFAPNNSVVNSNTMRIKGIVLFFSYAILLIIVIRTILRGIIKEME---LKSKEN 224
                                                                                                                                                                                                                                                                                                                                                                                        IESYNVI------PTLKFRKFVVIV-YLILFLILISFLSQYTKQKVQNEIMAQKEA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TTYMIEFAGIALSYLFLSVFNVDIGRLKDSLTKNKVKKRLIPMNITMLLYYLLIQVLYV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCIFMYLQTSDVVLSIS-----LPVAGCLIIIVWDYFLSVLYNYVFLVNQSVIKNDVSIH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GMIVITEIISLIFLM------LGWQQVTVMA-----
                                                                                                                                                                          KSNNFKIGLLQNIEVPEIKGMFSAKIIRAQETGIDVYIDVAESIKSFNMEIIDLSRVIGI
                                                                                                                                                                                                                  QDTRYNIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLÞEMELLDFITILSI 348
                                                                                                                                                                                                                                                                                                 QIRNITQYSQQIESLYKDIRSFRHDYLNILTSLRLGIENKDLASIEKIYHQILEKTGHQL
                                                                                                                                                                                                                                                                                                                                                                                                                                    WITFCIEFIGTYVTSRTIKKFVRD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 455; DB 2;
Pred. No. 1.6e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KFKAYNGHLKGTIGVVAAGTLILMLFV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g15022902; GSPDB:GN00168
ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----YLII 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                        404
                                                                                                                                                                          344
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                                                                                                                                                                                                                                                              284
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probable sensor histidine kinase ComD [imported] - Streptococcus pneumoniae (strain T C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001 C;Accession: B9261
B;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H A; blauws. r. A; blauws. R; blauws. R; blauws. A; Molecule type: DNA A; Residues: 1-441 < KUR> A; Cross-references: GB: AE005672; PI A; Cross-references: GB: AE005672; PI A; Cross-references: Strain TIGR4 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A;Authors: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95261 A;Status: preliminary K.E.; Paulsen, I.T.; Eisen, J.A.; White, O.; Salzberg, S.L.; Lewis, PIDN:AAK76283.1; PID:g14973747; GSPDB:GN00164; TIGR M.R.; Radune, D.; Holtzappl

A; Experimental source: strain C; Genetics:

Qy	Оy	Que Bes Mat	RESUI G9812 C;Spt C;Dat C;Dat C;Acc C;Acc C;Acc R;Hos	QУ	Qу	Qу Дь	ОУ ОЪ	Дb	P Qy	Ф	Qу	Quer Best Matc	A;Gene:
RRALIFFILDGTQGIVMGSSIITTYMIEFAGIALS	33 LSKKELTLFSISNFLIMIAVTMVNVNLFYPAEPLYFIALSTYLNRQNSLSLNIFYGLLPV 92 :::    :	Ouery Match  19.5%; Score 423.5; DB 2; Length 441; Best Local Similarity 25.9%; Pred. No. 1.3e-18; Matches 116; Conservative 84; Mismatches 171; Indels 77; Gaps 10;	RESULT 5  G98126 C;Species: Streptococcus pneumoniae C;Oate: 22-Oct-2001 *sequence_revision 22-Oct-2001 *text_change 02-Nov-2001 C;Accession: G98126 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E., LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; W. y. P.; Sun, P.M.; Winkler, M.E. J. Bacteriol. 183, 5709-5717, 2001 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Authors: preliminary A;Accession: G98126 A;Status: preliminary A;Molecule type: DNA A;Residnes: 1-441 <kur> A;Cross-references: GB:AE007317; PIDN:AAL00844.1; PID:g15459750; GSPDB:GN00174 C;Genetics: C;Keywords: phosphotransferase</kur>	403 GSNRGIGLAKVNHILEHYPKTSLÓTSNHHHLFKQLLIIK 441 	343 ITILSILCDNAIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKBNYSTK 402 :  : :  :   :	283 KTGHQLQDTRYNIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDE 342	223 MAQKEAQIRNITQYSQQIESLYKDIRSFRHDYLNILTSLRLGIENKDLASIEKIYHQILE 282 	167 MLLYYLLIQVLYVIESYNVIPTLK-FRKFVVIVYLILFLILISFLSQYTKQKVQNEI 222 	113 IVMGSSITTTYMIEFAGIALSYLFLSVENVDIGRLKDSLTKMKVKKRLIPMNIT 166 ::	59 LEYPAEPLYFIALSIYLNRQNSLSLNIFYGLLPVASSDLERRAIIFFILDGTQG 112	12 LLTYLTVLFLLFLESKVSNVTLSKKELTLFSISNFLIMIAVTMVNVN 58	Query Match 19.7%; Score 427.5; DB 2; Length 441; Best Local Similarity 25.9%; Pred. No. 7.6e-19; Matches 119; Conservative 99; Mismatches 188; Indels 53; Gaps 12;	ne: SP2236

RESULT AC1081 AC1081 sensor histidine kinase (AgrC from Staphylococcus) homolog Imo0050 [imported] - Liste Sensor histidine kinase (AgrC from Staphylococcus) homolog Imo0050 [imported] - Liste C:Species: Listeria monocytogenes C:Species: Listeria monocytogenes C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C:Accession: AC1081 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec. D: Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; A;Authors: Kreft, J.; Kuhn, M.; Fierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Authors: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Accession: AC1081 A;Status: preliminary A;Accession: AC1081 A;Residues: 1-431 GLA> A;Genetics: A;Genetics: AB107050
QY 414 NHILEHYPKTSLOTSNHHHLFKOLLIIK 441 : :    :  :  :  :  :  :   Db 410 KELLDKYNNIILETEMEGSTFROIIRFK 437
QY 354 TEAAFESLNPEIQLAFFKKNGSTVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIGLAKV 413 :  : :  : ::      : :      :  :  :  :
QY 294 NIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLÞEMELLDFITILSILCDNA 353       :   :  :  :  :
Qy 234 TQYSQQIESLYKDIRSFRHDYLNILTSLRLGIENKDLASIEKTYHQILEKTGHQLQDTRY 293  : :     :     :     ::  : :   : :     ::     :  :
Qy 184NVIPTLK-FRKFVVIVYLILELILISELSQYTKQKVQNEIMAQKEAQIRNI 233 :::  :     : :  :        : :  :
Qy 140 ENVDIGREKDSLTKMKVKKELIPMNITMELYYELIQVEYVYIESY
Db 69 GLYSYERWMKQYERDRGLFLSLLLSLLYESTHNFLSVTFSSTTGDNFVLQYHFPFF 124

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                                            Qy
                                                                                 200
                                                                                                                       Qy
                             DЪ
                                                                                                                                             В
                                                                                                                                                             Qy
                                                                                                                                                                                  Query Match 19.3%; Score 418.5; DB 2; Length 431; Best Local Similarity 26.8%; Pred. No. 2.6e-18; Matches 125; Conservative 88; Mismatches 142; Indels 111; Gaps
                            137 EKVNISRFYEHRKYAYIIFSIVALTVLAFYMNIYAGSIAGFDGSVLKINTLIFTGYTILL 196
                                                                 73 IYLNRQN-----SISLNIFYGLLPVASSDLFRRAIIFFILDGTQGIVMGSSIITTYMIEF 127
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ρy 밁 δã В

В

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D; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AD1438

A;Accession: AD1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: ADL438
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F.
D.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AL592022; PIDN:CAC95276.1; PID:g16412464; GSPDB:GN00178 A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-431 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: lin0043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sensor histidine kinase (AgrC from Staphylococcus) homolog lin0043 [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 VGYIDNNDMPGLKYYFENNIVPINKTIESNNYKISLLQNIHVIELKGLLAVKLIRAQELK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ILMAIIQITGIFIAIQILTNKVFSIKEGLVTIAIAMLAFPLFTLVQYWSMIFVLIVFVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSTKEKQIDVSKIFKENYSTKGSNRGIGLAKVNHILEHYPKTSLQT
                                                                                                                                                                                                    RIGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGHLANIQNDAVKGILSAKILEAQNKK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYWKNKNVIVSGSITLVVII-LLTISDS-----IVGFIL------VPG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLFLFSKVSNVTLSKKELT--LFSISNFLIMIAVTMVNVNLFYPAE--PLYFIAL----S 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSLPVNMPPIYKIFEEGFSTKGEGRGLGLASLREIMKKYSHVALDT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGHLANIQNDAVKGILSAKILEAQNKK 321
  NSTKEKQIDVSKIFKENYSTKGSNRGIGLAKVNHILEHYPKTSLQTS-NHHHLFKQLLII 440
                                                                                                                                                                                                                                                  IVIVTVVINTATNELKVQN----QKE-QLEQLQDYVTTLESLHREMRVFRHDYVNILSTL
                                                                                                                                                                                                                                                                                                                                                                                 ESYNVIPTLKFRKFVVIVYLILFLILISF ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGIALSYLFLSVFNVDIGRLKDSLTKMKVKKRLIP-----MNITMLLYYLLIQVLYVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYLNRQN-----SLSLNIFYGLLPVASSDLFRRAIIFFILDGTQGIVMGSSIITTYMIEF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDAILEVVEPIDKISMDSIDLCKVVGILLDNAVEAALTCENPVIRIAFVKKGDSIIIVFA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVIVTVVINTATNELKVQN----QKE-QLEQLQDYVTTLESLHREMRVFRHDYVNILSTL
                                                                IDAILEVVEPIDKISMDSIDLCKVVGILLDNAVEAALTCENPVIRIAFVKKGDSIIIVFA 371
                                                                                                              IAVNVEVSSKIQLPEMELLDFITILSILCDNAIEAAFESLNPEIQLAFFKKNGSIVFIIQ
                                                                                                                                                           VGYIDNDDMPGLKYYFENNIVPINKTIESNNYKISLLQNIHVIELKGLLAVKLIRAQELK
                                                                                                                                                                                                                                                                                                                                        EKVNISREVEHRKYAYIIFSIVALTVLAFYMNIYAGSIAGFDGSVLKINTLIFTGYTILL
                                                                                                                                                                                                                                                                                                                                                                                                                               ----LNFKYDEIFN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                           ---KOKVONEIMAQKEAQIRNITQYSQQIESLYKDIRSFRHDYLNILTSL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                               ------ELLPTLIYCAGMLANLLVFSFILRKL--I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 416; DB 2;
Pred. No. 3.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 112;
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Voss, H.; Wehland
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Fsihi, H.
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accessory gene regulator C [imported] - Staphylococcus aureus (strain N315) C:Species: Staphylococcus aureus C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C:Accession: D89995
                                                                                                                                                                                                                                                                       В
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A; Start codon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-83, 'T',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-423 <NOV>
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A;Cross-references: EMBL:X52543
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
R;Kornblum, J.; Projan, S.J.; Kreiswirth, B.N.; Mogazeh, S.L.; Eisner, W.; Ross,
submitted to the EMBL Data Library, March 1990
A;Reference number: S20793
A;Accession: S20797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Novick, R.P.; Projan, S.J.; Kornblum, J.; Ross, H.P.; Ji, G.; Kreiswirth, Mol. Gen. Genet. 248, 446-458, 1995
A;Title: The agr P2 operon: an autocatalytic sensory transduction system in A; Reference number: S58478; MUID:96004766
A; Accession: S58480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agrC protein - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 15-Oct-1999
C;Accession: S58480: S20797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X52543; NID:g46505; PIDN:CAA36783.1; PID:g581546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 FNVDIGRLKDSLTKMKVKKRLIPMNITMLLYYLLIQVLYVIESYNVIPTLKFRK-FVVIV 198
                                                                                                                             335 LDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHELFQESFSTKGEGRGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 Y-AYITKISDSIFVIFPSFFVVYVTISILFSYIINRVLKKIST----PYLILNKGFLIVI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 LSKKELTLFSISNFLIMIAVTMVNVNLFYPAEPLYFIALSIYLNRQNSLSLNIFYGLLPV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LNSYNFVLFVLTQMILMFTIPAIISGIKYSKLDYFFI-----
                                                                                                                                                                                                                                                                                             DTRYNIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDEITILSIL 349
                                                       LAKVNHILEHYPKTSLQT 427
                                                                                                                                                                                        CDNAIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIG 409
                                                                                                                                                                                                                                                              MNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVSSINLNMIDLSRSIGII
                                                                                                                                                                                                                                                                                                                                                                                        IETYYEYTLKIEAINNEMRKFRHDYVNILTTLSEYIREDDMPGLRDYFNKNIVPMKDNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STILLLTFSLFFFYSQINSDEAKVIRQYSLFYWYHYILSILTLYSQFLLKEMKYKRNQEE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STLSLE----LFKMFDSASLIILTSFIIIMYFVKIKWYSILLIMSSQIILYCANYMYIVI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSDLERRALIFFILDGTQGIVMGSSIITTYMIEFAGIAL-----SYLFLSV 139
LSTLKEIADNADNVLLDT 412
                                                                                                                                                                                                                                                                                                                                                                                                                       IRNITQYSQQIESLYKDIRSFRHDYLNILTSLRLGIENKDLASIEKIYHQILEKTGHQLQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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21.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 379; DB 2; Pred. No. 6.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ILISFLSQYTKQKVQNEIMAQKEAQ 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163;
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Oguc K.;

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C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89995
                                                                                                                                                                                                                                                                                                                         protein-histidine kinase homolog SapK - Lactobacillus sake (strain Lb706) plasmid pLSA6(C;Species: Lactobacillus sake C;Date: U3-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 15-Oct-1999 C;Accession: G56273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain N315 C; Genetics:
                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-428 <AXE>
                                                                                                                                                                                                       R;Axelsson, L.; Holck, A.
J. Bacteriol. 177, 2125-2137, 1995
A;Title: The genes involved in production of and immunity to sakacin A, a bacteriocin A;Reference number: A56273; MUID:95238285
A;Accession: G56273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: agrC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:BA000018; PID:g13701832;
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A; Residues: 1-371 < KUR>
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          A; Start codon:
                                A; Genome:
                                                     A; Gene: sapK; sakB
                                                                                                      A; Cross-references: GB:Z46867;
                                                                                      Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 RKFRHDYVNILTTLSEYIREDDMIGLRAYFNKNIVPMKDNLQMNAIKLNGIENLKVREIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 TLKFRKFVVIVYLILFLILISFLŞQYTKQKVQNEIMAQKEAQIRNITQYSQQIESLYKDI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 23.1 nes 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFTESENSVTFIVMNKCADDIPRIHELFQESFSTKGEGRGLGLSTLKEIADNADNVLLDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLITAKILRAQEMNIPISIEIPDEVSSINLNMIDLSRSIGIILDNAIEASTEIDDPIIRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSFRHDYLNILTSLRLGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGHLANIQNDAVK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMKYKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIAL-SYLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITMLLYYLLIQVLYVIESYNVIP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IALSIYLNRQNSLSLNIFYGLLPVASSDLFRRAIIFFILDGTQGIVMGSSIITTYMIEFA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TESSITELEEKLKYYAIVTI------LVTMIIMYLSNEATVGLELTLRKYTTDPA--
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23.5%; Pred. No. 1.5e-15;
tive 92; Mismatches 162;
                                                                                                      NID:g599849; PIDN:CAA86944.1; PID:g599854
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В Qy

120 LNNSATDITLL----GIFFAVLFDGLFFI---LLKNKRTELQHLNQEIIEFSLEK-QYFI 114 VMGSSIITTYMIEFAGIALSYLFLSVFNVDIGRLKDSLTKMK-VKKRLIPMNITMLLYYL 172

171

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RESULT
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A;Experimental source: strain Lb674
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A; Molecule type: DNA
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                                                                                                                               Matches 121;
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Best Local Similarity
                                                                                                                                               Query Match
Best Local .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 ILEHYPKTSLQTSNHHHLFK-QLLIIK 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 KALYNIHNEFVKSLIIAKIHQAKELNIECYCECQKPLDIVPIPIFDCIRILGILIDNAIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 GHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILCDNAIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 MIEFAGIALSYLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITMLLYYLLIQVL---YVI 180
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                                83
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60 VMVLMRLGWHFHQQKENKIKTTDTANLILIIVIQLLLVAVGTIISQFTISIIKSDFSQNI 119
                                                                                                                                               Local Similarity
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                                                                                             8 LSNGLLTYLTVLFLLFLFSKVSNVTLSKKELTLFSISNFLIMIAVTMVNVNLFYPAEPLY 67
                                                                6 VSVSLMQNFVAILLIFLLYRYIQRKITFKRIILD-----ILIAIIFSILYLFISDASLL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESYNVIPTLKFRKEV--VIVYLIL---FLILISFLSQYTKQKVQNEIMAQKEAQIRNITQ
                                FIAL-----SIYLNRQN------SLSLNIFYGLLPVASSDLFRRAIIFFI-LDGTQGI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AASECNEKILYLVIYQDDLQIEFSIKNTYKKSNMSIGTLQRKNISTKKGHSGLGLNTIQE
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                                                                                                                                               16.0%;
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                                                                                                                                             Score 348; DB 2;
Pred. No. 5.3e-14;
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Pred. No. 7e-15;
                                                                                                                               Mismatches
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                                                                                                                                                           Length 448;
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A;Cross-references: GB:AE001437; PIDN:AAK79549.1; PID:g15024536; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: B97095
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J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl A;Reference number: A96900; MUID:21359325; PMID:21359325
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A; Residues: 1-452 < KUR>
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                                                                                                                                                                        261 LRLGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGHLANIQNDAVKGILSAKILEAQNK 320
                                                                                                                                                                                                                                                                                        208 SFLSQYTKQKV-----QNEIMAQKEAQIRNITQYSQQIESLYKDIRSFRHDYLNILTS
                                                                                                                                                                                                                                                                                                                                                     164 YKQLYLVMPCISIYGISFLF----YNVQLVDTGKGEYYLPEIFSSIYCMLPFIGLFLILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 FINKD-----YLKIFNLILINFRDILNEIFLFMLLKCICSILKIKNS--ELNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 IITTYMTEFAGIALSYLFLSVFNVDIGRLKDSLTK-------MKVKKRLIPMNI 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YPAEPLYFI--ALSIYLNRQNSLSLNIFYGLLPVASSDLFRRAIIFFILDGTQGIVMGSS 118
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----GIELYCDFIMPEKAGIEPIDLSIILNNSLDNAIEACRKIKNLELHKRISIKSIVKN 385
                                                                                                                     LR----NLAYSDNI--DVLKNYLNNISETIKKLDFIIKTGNAVADAVINEKYTIAKNE
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21.6%;
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C; Geneti
A; Gene:
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1533
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A;Mosidues: 1-433 <GLA>
A;Residues: 1-433 <GLA>
A;Cross-references: GB.AL592022; PIDN:CAC96034.1; PID:g16413253; GSPDB:GN00178
A;Experimental source: strain Clip11262
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Science 294, 849-852, 2
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AB1533
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                                               385 KE-KQIDVSKIFKENYSTKGSNRGIGLAKVNHILEHY 420
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                                                                                                               CEINVPNDI-DVVPFDLSTVLGNLIDNAAEALEYVQNEKWIGIKISYQVGFLMIQVANSF
                                                                                                                                                                         VEVSSKIQLPEMELLDFITILSILCDNAIEAAFESLNPE-IQLAFFKKNGSIVFIIQNST
DGIVHLDNKKIISRKEDTE--NHGIGLTSIKKIAGKY 412
                                                                                                                                                                                                                                                                                        IEKIYHQILEKTGHQLQDTRYNIGHL-----ANIQNDAVKGILSAKILEAQNKKIAVN
                                                                                                                                                                                                                                                                                                                                                     IEKMVKTQVDSKVLDEKNKYYEQQLVTMKQTLESQRTVRHDLKNKLSPL---IYLAESGK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGNGSLPTIYWTTFLFITMKDILWVLILADSPVEISFYYWAAVIPLLPVSYILFYYTRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L----MSLTSTAIGR------QDVGEFMLQPSNTMLLFTISRLISLGLVLIILRFRKIR 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEYLLIYFLESRYKPMNPRVSKEKLILIFCIASL-----VQAFFDSEE-YF----
                                                                                                                                                                                                                                  TDELVEQVQE------LGSLSVLGKIYADSGNITIDYIINLKLQALANKGYTIF
                                                                                                                                                                                                                                                                                                                                                                                                        VQNEIMAQKEAQI--RNITQYSQQIESLYKDI---RSFRHDYLNILTSLRLGIENKDLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----IPTLKERKEVVIVY--LILFLIL-----ISE-------LSQYTKQK
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two-component sensor histidine kinase citS - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000 C;Accession: E69600

E69600

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                                                                                                                                                                                                                                                                                                                                                                     two-component sensor histidine kinase BH0397 [imported] - Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: E83699
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A;Gene: citS
C;Superfamily: two-component sensor histidine kinase; sensor histidine kinase homology
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; pMID:11058132
A;Accession: E83699
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A;Status: preliminary
A;Molecule type: DNA
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A;Experimental source: strain 168;
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A; Residues: 1-542 < KUN>
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97; Conservative
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A;Residues: 1-532 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04116.1; GSPDB:GA;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0397
C;Superfamily: two-component sensor histidine kinase; sensor histidine kinase homolog
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Best Local Similarity
                                                                                                                                                                                                                       413 IPKASSEQMVHELITILGNLIDNALEAVIKA
                                                                                                                                                                                                   299 IVNDEVVGAISTFRDLTEIKQQAKQLTGVKLYVEALRAQSHEFMNKLHVILGMVKTESYD
                                                                                                                         359 ELNDYIHQIVNHRSTELNHV-----IKRIKDSVLAGFILGKLSYAREKHITLDVQTKSV
                                                                                                                                                           272 SIEKIYHQILEKTGHQLQDTRYNIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSK 331
DV-----SKIFKENYSTKGSNRGIGLAKVNHILE 418
                                                                     IQLPEMELL--DFITILSILCDNAIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQI 389
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                           7.9%;
24.0%;
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                                                     -KEKTVLVQLEYSNERLHI 461
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Search completed: July 30, 2002, 15:15:20 Job time: 391 sec

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RVQDTGPGIPDGEQGDIFKKGYSTKGENRGYGLYLVKQSVE 502

7 escherichia
6 bacillus su
6 bacillus su
3 esicharomyc
3 epifagus vi
3 mycoplasma
7 buchnera ap
5 marchantia

methanococc

5 porphyra pu 2 saccharomyc 5 schizosacch 7 mycoplasma

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Post-processing: Minimum Match 0%,
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
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SURA_BUCAI
                  CAPE_STAAU
BXF_CLOBO
ALP1_SCHPO
TRME_LACLA
                                                                                           YFHK_ECOLI
MUS2_BORBU
NU2M_PODAN
RASO_ARCFU
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YC26_PORPU
DP01_ANATH
YGIY_HAEIN
COX1_ACACA
NIST_LACLA
NIST_LACLA
TLR3_HUMAN
Y976_METJA
Y61_METJA
Y61_MESVI
YHL6_YEAST
Y58_BUCAI
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  REAL BARRES BARR
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P39272; P76795;
Ol-FEB-1995 (Rel. 31, 'Created)
Ol-NOV-1997 (Rel. 35, Last sequence update)
Ol-MAR-2002 (Rel. 41, Last annotation update)
Sensor protein dcus (EC 2.7.3.-).
DCUS OR B4125 OR Z5727 OR ECS5107.
                                STRAIN=K12 / MC4100;
MEDLINE=98440434; PubMed=9765574;
MIDININE=98440434; PubMed=9765574;
Zientz E., Bongaerts J., Unden G.;
Tummarate regulation of gene expression in Escherichia
DcusR (dcusR genes) two-component regulatory system.";
D. Bacteriol. 180:5421-5425(1998).
                                                                                                                                                                                                 STRAIN-0157:H7 / RIMD 0509952;

MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogsawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genome sequence of enterohemorrhagic Escherichia Coli "Complete genome comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                           Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12 / MG1655;
MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, So
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STRAIN=K12 / 1
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  CHARACTERIZATION, AND TOPOLOGY
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Tobe T.,
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Result

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Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004358; BCTRLSENSOR.
InterPro; IPR003594; HATPase_c.
InterPro; IPR004359; HIS_KIN_sig.
InterPro; IPR000014; PAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; pF00989; pAS; 1.
pfam; pF00512; signal; 1.
pRINTS; pR00344; BCTRLSENSOR
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MEDLINE=99138745; Pu
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Bacteriol. 181:1238-1248(1999).
FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane. MISCELLANDOUS: THE REGION ENCOMPASSING APPROXIMATELY RESIDUES 42 TO 181 HAS BEEN SHOWN TO BE PERIPLASMIC, HOWEVER EXACTLY WHICH RESIDUES ARE PERIPLASMIC IS NOT CLEAR.
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RESULT 2
KINB_BACSU
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                                                                                                                                                                                                                                                                                                                             MEDLINE=97419515; PubMed=9274030;
Oudega B., Koningsteijn G., Rodrigues L., de Sales Ramon M.,
Hilbert H., Duesterhoeft A., Pohl T.M., Weitzenegger T.;
"Analysis of the Bacillus subtilis genome: cloning and nucleotide
"sequence of a 62 kb region between 275 degrees (rrnB) and 284 degrees
                                                                                                                                                                                                                               Microbiology 143:2769-2774(1997).

-i- FUNCTION: PHOSPHORYLATES THE SPORULATION-REGULATORY PROTEINS SPOOM AND SPOOF. SPOOF IS REQUIRED FOR THE KINB ACTIVITY.

-i- SUBCELLULAR LOCATION: Integral membrane protein.

-i- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
01-MAR-2002
SubtiList; BG10745; kinB
          EMBL; Z93933; CAB07911.1; -.
EMBL; U63302; AAB61980.1; -.
EMBL; Z99120; CAB15134.1; -.
PIR; S32935; S32935.
                                                                                              entities requires a or send an email to
                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dartois V.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Multisensory activation of the phosphorelay initiating sporulation in Bacillus subtilis: identification and sequence of the protein kinase of the alternate pathway.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus group; Bacillus NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sporulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      008430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINB_BACSU
                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trach K.A., Hoch J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93268102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 8:69-79(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 L-GGSIAVESEPGIFTQFFV 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 VIAGFLISKINRATD--LGHTLILNSESQLPDSGSEDQVATLITTLGNLIENALEALGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 ALRERSHEFMNKLHVI-LGLLH--LKSYKQLEDYIL-KTANNYQE---EIGSLLGKIKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 DIRSTRHDYLNILTSLRLGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGH-LANIQND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---EIQLAFFKKNGSIVFIIQNSTKEKQID-VSKIFKENYSTKGSNRGIGLAKVNHILEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPKTSLQTSNHHHLFKQLLI 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGGEISVTLHYRHGWLHCEVNDDGPGIAPDKIDHIFDKGVSTKGSERGVGLALVKQQVEN
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                                                                                                an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 30, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
kinase B (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Djavakhishvili T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=8497199;
                                                                                                            license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoch J.A.
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Best Local
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              DCTS_BACHD
Q9K997;
16-OCT-2001
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TRANSMEM
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TRANSMEM
DOMAIN
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Pfam; PF00512; signal; 1.
SMART; SM00387; HATPase_c; 1.
SMART; SM00388; Hiska; 1.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                      373
                                                                                                                          391 VSKIFKENYSTKGSNRGIGLAKVNHILEHYPKT 423
                                                                                                                                                   314 DLLIYGDATKLKQAVINLMKNSIEAVPHGKGMIHIS-AKRNGHTIMINITDNGVGMTDHQ 372
                                                                                                                                                                                                                                                                                                  156 ALNI---LNFOKSGIFYYEAAVSGLFRSSVLLLSIYIIESIAENI-----ALRSQLIHS
                                                                                                                                                                                                                                                                                                                         182 SYNVIPTLKERKEVVIVYLI----LELILISELSQYTKQKVQNEIMAQKEAQIRNITQYS
                                                                                                                                                                                                                                                                                                                                                                         124 MIEFAGIALSYLFLSVFNVDIGRL--KDSLTKMKVKKRLIPMNITMLLYYLLIQVLYVIE 181
                                                                                                                                                                                                                                                                                                                                                 96 LIFYEPSAMFVFTLLPFLIIIPILFQKKWPFMSKAKKLLLSLLISCVEIFLFFASSWILS 155
                                                                                                                                                                                                                                                                                                                                                                                                   60 MDYIQ-----YGLQMIPV-----IICLFYISTASGLTVAASVLCFE
                                                                                                                                                                                                                                                                                                                                                                                                                          66 LYFIALSIYLNRQNSLSLNIFYGL--LPVASSDLFRRAIIFFILDGTQGIVMGSSIITTY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ILKDYLLHICFILFPILLYQV---+FWLGKPAILVPKINSGLVTLFACGASVLCIIFPIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 ILSNGLLTYLTVLELLELESKVSNVTLSKKELTLESISNELIMIAVTMVNV-NLFYPAEP
                                                                                                    MOKLGEPYYSLKTNGTGLGLTVTFSIIEHHHGT 405
                                                                                                                                                                          EMELLDFITILSILCDNAIEAAFESL---NPEIQLAFFKKNGSIVF--IIQNSTKEKQID
                                                                                                                                                                                                 -----GIITNYLDMAKQQLYEKEVFDLSALIKETSSLMVSYANYKSVTVEAETE---P
                                                                                                                                                                                                                           QDTRYNIGHLANIQNDAVKGI-----LSAKILEAQNKKI-----AVNVEVSSKIQLP
                                                                                                                                                                                                                                                  EKMTIVSELAASVAHEVRNPLTVVRGFVQLLFNDETLQNKSSADYKKLVLSELDRAQ----
                                                                                                                                                                                                                                                                          QQIESLYKDIRSFRHDYLNILTSLR-----LGIENKDLASIEKIYHQILEKTGHQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003594; HATPase_c.
IPR004359; HIS_KIN_sig
IPR003661; His_kinA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
38
58
69
90
100
121
133
154
1188
218
(Rel. 40, Created)
(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.4%; |Score 139; DB 1; Length 428; 20.5%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLETE PROTEOME.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FACGA -> SSPAAP (IN REF. 1 AND 3).
MISSING (IN REF. 2).
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CYTOPLASMIC (POTENTIAL).
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POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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EXTRACELLULAR (POTENTIAL)
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                                        PRT;
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                                        532 AA
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Best Local S
Matches 97
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20512582; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bactleria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (Rel. 41, Last annotation update) Probable C4-dicarboxylate sensor kinase (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50112; PAS; FALSE_NEG.
Sensory transduction; Transferase; Kinase; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00344; BCTRLSENSOR. SMART; SM00387; HATPase_C; 1. SMART; SM00091; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004359; HIS_KIN
InterPro; IPR000014; PAS.
Pfam; PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          halodurans and genomic sequence comparison with Bacillus Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takami H.,
Fuji F., H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=86665;
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                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                      RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004358; BCTRLSENSOR. InterPro; IPR003594; HATPase_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of the alkaliphilic bacterium Bacillus
127 -- FAG--IALSYLFLSVFNVDIGRLKDSLTK-----
                                 138
                                                               84
                                                                                                                              40
                                                                                              08
                                                                                                                                                             24
                                                                                                                                                                                           4 ALMILSNGLLTYLTVLFLLFLFSKVSNVTLSKKELT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN. SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR PROBABLY ACTIVATES DCTR BY PHOSPHORYLATION. ESSENTIAL FOR EXPRESSION OF DCTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR BH2752
                                                                                                                                                          ALMMVSISLLGYVTSI----KEDELSNRTMITAQLVAQNHTVQQWVDAKPEEASRTLQPI 79
                               VTVRAFMPILNQQ--REQV------GVAVVGSVLPSYADMIQEFWQPALLIGLITAL 186
                                                               NIFYGLLPVASSDLFRRAIIFFILDGTQGIVMGSSIITTY -- MIE------
                                                                                              VERIRVINDHDYIVLLNMDRIRITHPIPERLQTPFVGGDEDPAF--AEHIYLSKAKTEGV 137
                                                                                                                              ---LFSISNFLIMIAVTMVNVNLFYP-----AEPLYFIALSIYLNRQNSLSL 83
                                                                                                                                                                                                                          l similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20512582; PubMed=11058132;
L., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
                                                                                                                                                                                                                                         18.48;
                                                                                                                                                                                                                                                                                                      59999 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteome
                                                                                                                                                                                                                          99;
                                                                                                                                                                                                                                         Score 129.5; D
Pred. No. 0.74;
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                                                                                                                                                                                                                                                                                                                                       HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC
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                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                          173;
                                                                                                                                                                                                                                                       Length 532;
                                                                                                                                                                                                                          Indels 159;
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01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Gerlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou J

Overbeek R., Gocayne J.D., Weldman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M. Olson G. T. Fracer M. Gmith U. Grand D.,
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            Venter J.C.; "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; Nature 390:364-370(1997).

-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat Hypothetical protein AF1421.
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                                                   TRANSMEM 19 41

    -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
    -i- SIMILARITY: BELONGS TO THE UPF0182 FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                       Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaeoglobus fulgidus.
                                                                                            TIGR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDFLKIRVRDNGEGIREEVREKMEVRGFSTKSTSGRGIGLFLIQAIVE 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQNKKIAVNVEVSSK-IQLPE-MELLDFITILSILCDNAIEA--AFESLNPEIQLAFFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAGLIQLDEGKKALQYIFDLEEEQEEFSGVVMQ~---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGSIVFIIQNSTKEKQIDV-SKIFKENYSTKG-SNRGIGLAKVNHILE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKELGYQYIJEKDSEFIDHPEGYTTHDLYYIYGNLIDNSLDAFSSTQDQNKTVHYFIGEE
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                                                                                            AE001005; AAB89825.1; AF1421; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                       Transmembrane;
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Matches
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SEQUENCE
                                                                                                                                                                                           DPIB_ECOLI STANDARD; PRT; 552 AA.
P77510; O54338;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Sensor kinase dpile (EC 2.7.3.-) (Sensor kinase citA).
DPIB OR CITA OR MPDB OR B0619.
        ingmer H., Miller C.A., Cohen S.N.;
"Destabilized inheritance of pSC101 and other Escherichia coplasmids by DplA, a novel two-component system regulator.";
Mol. Microbiol. 29:49-59(1998).
                                                                      SEQUENCE FROM N.A.,
STRAIN=K12 / MG1655;
MEDLINE=98367124; Pu
                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                              Escherichia coli
                                                                                                                                  NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVFLTYLKHSLGFFFL------EFIIFFVPLFLTNVAVR--KVTLEFHGEPLKI 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNLH-DVKLQKFDYWDVVNYNDI-LEAKDTIDNIRIWDHRPIRDVFRQLQQIRTYYVIQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLKIVIG-SLLAALLISLAIAAFAYMYAF-----RWVKSLEEF----KEIFPGSGFMHF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHLADFGIAFFAALTV----KNYWSSMLFY----FNSSNFGVSDPIFGIDAAFYTFQLP 148
                                                                                                                                                                                                                                                                                                                                                                                                                         KGDV-----NFFTKYAGDGGIKLDYFRKVLFSFRFGDINLILSNYITDESRLMMHRDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDVDRYRI-----NDSYVQLLLAARELSTENLPSRAQTWLNKHLIYTHGYGIVASPVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 20.
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                 538
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                                                                      PubMed=9701802;
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259 PO
290 PO
102210 MW;
                                                                                                     AND CHARACTERIZATION
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Pred. No.
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N; 8AD99AB7B4E50671 CRC64;
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                                                                                                                                                                   Enterobacteriaceae;
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Ptam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR,
SMART; SM00387; HATPase_C; 1.
SMART; SM00091; PAS; 1.
PROSTRO. NGEGTO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yano M., Horiuchi T.;

"A 718 kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).

-1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DPIA/DPIB ESSENTIAL FOR EXPRESSION OF CITRATE-SPECIFIC FERMENTATION GENES AND GENES INVOLVED IN PLASMID INHERITANCE. MAY ACTIVATE DPIA BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kitura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yapo M., Horiuchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-KI2 / MG1655;

STRAIN-KI2 / MG1655;

MEDLINE-97426617; PubMed-9278503;

Blattner F.R., Plunkett G. TII, Bloch C.A., Perna N.T., Burland V.,

Blattner F.R., Plunkett G. TII, Bloch C.A., Perna N.T., Burland V.,

Blattner F.R., Plunkett G. TII, Bloch C.A., Poena N.T., Mayhew G.F.,

Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                           ECOGene; EG13546; dpiB.
InterPro; IPR004358; BCTRLSENSOR.
InterPro; IPR003594; HATPASSe_c.
InterPro; IPR004359; HIS KIN_sig.
InterPro; IPR000014; PAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                     PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 HASTIDINE KINASE DOMAIN. SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                        U82598;
D90702;
                                                                                                                                                                                                                                                                                                          PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                          PF00989; PAS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U46667; AAC28951.1; -. |
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PS50112; PAS; FALSE_
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183
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347
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BAA35255.1; -. |
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                     HISTIDINE KINASE
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RESULT 6
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ID CHVG_R
AC P72292
DT 30-MAY
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DT Sensor
DE EXOS).
GN Rhizob
OC Rhizob
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P7222; 031069;
30-MAY-2000 (Rel. 39, C
01-MAR-2002 (Rel. 41, I
01-MAR-2002 (Rel. 41, I
                                                      MEDLINE-21396507; pubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Boistard P., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
'Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.",
                            Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Sensor protein chvG (EC 2.7.3.-) (Histidine kinase sensory protein
Proc. Natl. Acad. [3]
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                                                                                                                                                                                                                                                                                                                                                                                    Cheng H.-P., Walker G.C.;
"Succinoglycan production by Rhizobium meliloti is regulated through
the ExoS-ChvI two-component regulatory system.";
J. Bacteriol. 180:20-26(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHVG OR EXOS OR R00043 OR SMC04446.
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SEQUENCE FROM N.A.
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Best Local
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Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00304; HAMP; 1.
SMART; SM00387; HATPase_c; 1.
SMART; SM0038B; HiskA; 1.
                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96032383; PubMed=7559334;
Oesteraas M., Stanley J., Finan T.M.;
"Identification of Rhizobium-specific intergenic mosaic elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-112 FROM N.A. STRAIN=SU47 / 1021;
                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          within an essential two-component regulatory system of Rhizobium
                                                                                                                                                                                                                                                                                                   MOD_RES
                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sensory transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                      272 LYNVILSLLLSSTIANPLRRLSAAAIRVRRGGAKEREEIPDFSSRQDEIGNLSVALREMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: EXOPOLYSACCHARIDE BIOSYNTHESIS.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: MEMBER OF A TWO-COMPONENT REGULATORY SYSTEM CHYG(EXOS)/CHYI INVOLVED IN REGULATING THE PRODUCTION SUCCINOGLYCAN. ACTIVATES CHYI BY PHOSPHORYLATION.
                                                                                                                                                              IVYLILELILISELSQYTKQ-------KVQNEI--MAQKEAQIRNITQYSQQIE
                              RLDRLISDISDASR---LDAELARADAKKVDLEKLLGDLVEISRQIRGSKKPVLLDFVVDR
                                                        NIGHLANIQNDAVKGILSAKILEAQNKKIAVN---
                                                                                  TALYDRIAAIENFAADVSHELKNPLTSLRSAVETLPLARNEESKKRLMDVIQHDVR----
                                                                                                          SLYKD----IRSF----RHDYLNILTSLRLGIENKDLASIEKIYHQILEKTGHQLQDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF027298; AAB96631.1; -.
AL591782; CAC41430.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U32941;
                                                                                                                                                                                          68;
                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                PS50109; HIS_KIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003660; HAMP.
IPR003594; HATPase_c.
IPR004359; HIS_KIN_sig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003661; His_kinA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR004358; BCTRLSENSOR.
                                                                                                                                                                                                                                                          30
51
261
282
282
347
350
136
266
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; HAMP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB07686.2;
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                                                                                                                                                                                                                                                                                                                                                                                                        Inner membrane; Exopolysaccharide synthesis;
                                                                                                                                                                                                                                                                                   29
260
281
577
575
350
                                                                                                                                                                                                                                                            266
63720
                                                                                                                                                                                                     5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; Kinase; Phosphorylation;
ILSILCDNAIEAAFESLNPEIQLAFFKKNG-----
                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                          57;
                                                                                                                                                                                       Score 127; DB Pred. No. 1.1; 57; Mismatches
                                                                                                                                                                                                                                                                         ٦ ٢
                                                                                                                                                                                                                                                                                                                        PERIPLASMIC (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                              HISTIDINE KINASE
                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                      -> F (IN REF.
                                                                                                                                                                                                                                                            BEF2DD4A4F0E2B15 CRC64;
                                                      ---VEVSSKIQ-LPEMELLDFIT--
                                                                                                                                                                                                                  ۲.
                                                                                                                                                                                          ; 68
                                                                                                                                                                                                                  Length 577;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions
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P96601;
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50112; PAS; FALSE_NEG.
Sensory transduction; Transferase;
                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98000887; PubMed=9341680; Beloin C., Ayora S., ExLey R., Hirschbein L., Ogasawara N., Beloin C., Alonso J.C., Le Hegarat F.; Kasahara Y., Alonso J.C., Le Hegarat F.; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."; "Characterization of an Irp-like (IrpC) gene from Bacillus subtilis."
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16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Probable C4-dicarboxylate sensor kinase (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACSU
                                                                InterPro; IPR004359; HIS_KIN_sig.
InterPro; IPR000014; PAS.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF09512; signal; 1.
SMART; SM00387; HATPase_c; 1.
SMART; SM00387; PAS; 1.
                                                                                                                                                                                                          SubtiList; BG12073; dcts.
InterPro; IPR003594; HATPase_c
                                                                                                                                                                                                                                                         EMBL; AB001488; BAA19282.1; -. EMBL; Z99106; CAB12252.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbiology 146:263-271(2000).
-I- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR. PROBABLY ACTIVATES DCTR BY PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Staphylococcus
NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20170658; PubMed=10708364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Regulation of the transport system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION, AND GENE NAME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN. SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESSENTIAL FOR EXPRESSION OF DCTP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogasawara N., Yoshikawa H., Danchin A.; (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus
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  Kinase; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
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                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 S., Ogasawara 1
C4-dicarboxylic
                                                                                                                                                                                                                                                                                                                                                                   Usage
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Best Local
                                                                                                                                                                                                                                  P37608:
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Lacticin 481/lactococcin transport ATP-binding protein lcnDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
SEQUENCE
subsp. lactis.";
Appl. Environ. Microbiol. 60:1652-1657(1994).
-i- FUNCTION: PROBABLY IMPLICATED IN THE EXPORT PROCESS OF THE
                                                                                                                                                                                                                                                                                                                                                LACLA
                                                                                                                        STRAIN-ADRIA 85L030;
MEDLINE-94288641; PubMed-8017945;
                                           "Cloning, expression, and nucleotide sequence of genes involved in production of lactococcin DR, a bacteriocin from Lactococcus lactis subsp. lactis."
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                             Bacteria; Firmicutes;
                                                                                                                                                                                                                             Lactococcus lactis (subsp. lactis) (Streptococcus lactis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation;
                                                                                                             Rince A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                             Pennec J.P
                                                                                                                                                                                  NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                  CN3_LACLA
                                                                                                                                                                                                                                                                                                                                                                                                        486 KTGGTGYGLYLVKQIIDKGSGT-TEVDSH 513
                                                                                                                                                                                                                                                                                                                                                                                                                                     402 KGSNRGIGLAKVNHILEHYPKTSLQTSNH 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 SILCDNAIEAAFESLNPE---IQLAFFKKNGSIVFIIQ-NSTKEKQIDVSKIFKENYS-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 EQENVTEFLHRSIQNDAAAGLLLSKIRRGRELGIAVHIDENSSLQQFPEHVDQHDIVVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 VLYVIESYNVI-----PTLKFRKFVVIVYLILFLILISFLSQYTKQ--KVQNEIMAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 -----PGIADILLHLKRDIAFIVVLTLGFGLAGSFLLARHIKKQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 YMIEFAGIA--LSYL----FLSYFNVDIGRLKDSLTKMKVKKRLIPMNITMLLYYLLIQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AEHIYFSE----AKGEIGTAVRAFY---PVKDQDLNQIGV-----VLVGKTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 AEPLYFIALSIYLNRQNSLSLNIFYGLLPVASSDLFRRAIIFFILDGTQGIVMGSSIITT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRYNIGHL--ANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKI-QLPE-MELLDFITIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNLIENAF-GSFETVQSEDKRIDISIEQTDDILAILIEDNGCGIEPTHMPRLYDKGFTVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----IRSF----RHDYLNILTS----LRLGIENKDLASIEKIYHQILEKTGHQLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVLKDSRLPEIVERNKAVYNEEIRVSGKVIMSSRIPIVMKKKVIGAVAIFQDRTEAAKMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ~MFQLEPHEIVRMYEERTATFHSMNEGVIAIDNRLVITIFNEKAKQIFEVQGDLIGKVIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 18.7
84; Conservative
                                                                                                         Dufour A., le Pogam S., Thuault D., Bourgeois C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59942 MW;
                                                                                                                                                                                                           Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (AUTO-) (BY SIMILARITY).; 614BDA8BE8F10CFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 137;
                                                                                                                                                                                                                                                                                                                                691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00664; ABC_membrane; 1. Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00382; AAA; 1. PROSITE; PS00211; ABC_T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U91581; AAC72259.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003593; AAA. InterPro; IPR003140; ABC_transporter InterPro; IPR003149; ABC_transportr. InterPro; IPR003439; ABC_GTP_A.
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591 GKNLSGGQIQRLLIAKSLLNNNKFIFWDEPFSSLDNQNRIHIYKNVL
                                                                                                                                             472
                                                                                                                                                                                                                 412
                                                                                                                                                                                                                                                    283
                                                                                                                                                                                                                                                                                        355
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                                                                                                                                                                                                                                                                                                                                                                                                                                     249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 VMGSSIITTYMIEFAGIALSYLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITMLLYYLL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 QKNTNLLY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 TFL-YIFSLFISQIVALWFSIILRDILNKSHDITYS---FIMMISLVLFQTLSLLMKLGA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 --NVNLFYPAEPLYFIALSIYLNRQNSLSLNIFYGLLPVASSDLFRRAIIFFILDGTQGI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 TYLTVLFLLFL-----FSKVSNVTLSKKELTLFSISNFLIMIAVTMV------ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LANTIBIOTIC LACTICIN 481/LACTOCOCCIN DR.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. HLYB SUBFAMILY.
                                                                                                                                                                                                                                                    KTG-----HQLQDTRYNIGHLA-----
                                                                                                                                                                                                                                                                                                                         TQYSQQIESLYKDIRSF-----RHDYLNILTSLRLGI--ENKDLASIEKIYHQILE 282
                                                                                                                                                                                                                                                                                                                                                            MNLLYMIFSFSLI---SIKRQANIQYTQQTIDFTSVVQEDLNQIEQIKAQANEKECVKRW
                                 GSNRGIG-----LAK--VNH---ILEHYPKTSLQTSNHHHLFKQLL 438
                                                                      GVVSQNMNLRKGSLIENIVSNNNSEELDIQKINDVLKDVNMLELVDSLPQKIFSQLFE-N
                                                                                                         QLAFFKKN---GSIVFIIQNSTKEKQIDV------
                                                                                                                                             SYELNNYIFNNINFSIKKGEKIAIVGKSGSGKSTLFNILLGLISYEGEVTYGYENLRQII
                                                                                                                                                                                                                 QSGISLFVSAVNQIQDVMFEISRLSIYGNKISDLLIENPQRIDNIEKHSNNAIILKDISY
                                                                                                                                                                                                                                                                                        TKKSAQTIFSYNKILNIDGITSAFNQGFNYICVILMMIFGIYLNQGNLVSIPDL---IIF
                                                                                                                                                                                                                                                                                                                                                                                                IQVLYVIESYNVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQIRNI
                                                                                                                                                                                                                                                                                                                                                                                                                                     IIEKINLRTGIRD--GILLK-IFPSLLNF-----FTVFIVIIYLGTISFTLTLFLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
                                                                                                                                                                              -LEAQN---KKIAVNVEVSSKIQLPEMELLDFITILSILC----DNAIEAAFESLNPEI 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABC_TRANSPORTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%;
19.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 126.5;
Pred. No. 1.
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4276DD778AEC0B47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                           ----SKIFKENYSTK 402
                                                                                                                                                                                                                                                    -NIQNDAVKGILSAKI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 691;
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                                                                                                                                                                                                                                                                                                                                                              354
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NTP2_MSEPV
                                                                                                                                                                                                                                                                                  Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00690; DEAH_Arr__NLT_______Transcription ATP-binding; Helicase; HydroLase Helicase.

DOMAIN 328 533 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;

"The genome of Melanoplus sanguinipes entomopoxvirus.";

"Virol. 73:533-552(1999).

"Virol. 73:533-552(1999).

"I VIROL 73:533-552(1999).

"I VIROL 73:533-552(1999).

"I VIROL 73:533-552(1999).

"I VIROL 73:531-552(1999).

"I VIROL PARSUMABLY BY PREVENTING ROLE

"I VIROL PARSUMABLY BY PREVENTING RE-

"I VIROL PARTICLES OF THE EXPORT OF THE CYTOPLASM.

"I VIROL PARTICLES (BY SIMILARITY).

"I CATALYTIC ACTIVITY: NTP + H(2)0 = NDP + phosphate.

"I SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nucleoside triphosphatase II (EC 3.6.1.15) (NTPase II) (Nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTP2_MSEPV STANDA:
Q9YW06;
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melanoplus sanguinipes entomopoxvirus Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF063866; AAC97810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Tucson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=83191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                triphosphate phosphohydrolase II) (NPH II).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99102612; PubMed=9847359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                160 LIPMNITMLLYYL ---
                                                                                                                                                                        75
                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                15 YLTVLFLLFLFSKVSNVTLSKKELTLFSISNFLIMIAVTMVNVNLFYPAEPLYFIALSIY 74
MIDVQLKIFEIFISKKNCIISGGTGIGKTTVIPKLFWWFNLLFDGYEFWNTSNENKNIND
                                                                                                                                                                        LNR-----QNSLSLNIFYGLLPVASSDLFRRAIIF----FILDG------
                                                                                                                                                                                                              YNYMAYLLF ---- PNNATIFNSYITKKEVFEYPMQFAIAL ----- YPVYKLYWHNINIC 75
                                                                    VTIISQITINISSLNKYQIYGIIESANYLGILSSYKQNKYFDKNL----FSFTKSELRST
                                                                                                    ---TQGIVMGSSIITTYMI-----EFAGIALSYLFLSVFNVDIGRLKDSLTKMKVKKR 159
                                                                                                                                        LNNRFIYLSNEFKNNISINTYYNL------LYNNELKFEDDNIIINGKNLKISYSAYSY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00490; HELICC; 1.
E; PS00690; DEAH_ATP_HELICASE; FALSE_NEG
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002464; DEAH_ATP_helicase
IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001410; DEAD
                                                                                                                                                                                                                                                                                                                                                                   206
331
717 /
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                       ΑA,
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                                                                                                                                                                                                                                                                                                                                                                     334 I
84725 MW;
                                                                                                                                                                                                                                                                                                 5.8%;
18.3%;
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                                                                                                                                                                                                                                                                                  97;
                                                                                                                                                                                                                                                                                                   Score 125.5;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                      DEXH BOX
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                                                                                                                                                                                                                                                                                                                                                                       E8FB04661F1EA863 CRC64;
                                                                                                                                                                                                                                                                                Mismatches 172;
                                  ---LIQVLY-----VIESY--
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Poxviridae;
                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                  Indels 209;
                                                                                                                                                                                                                                                                                                                  Length 717;
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                                                                                                                                                                                                                                                                                  Gaps
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RESULT 10
V120_HSV7J
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                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P52438;
01-OCT-1996
01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                    EMBL; U43400; AAC54692.1; -. Capsid assembly. SEQUENCE 938 AA; 110170 M
                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
EHV-1 23, EBV BOLF1, VZV 21, HVS-1 63, AND HCMV UL47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human herpesvirus (type 7 / strain JI) (HHV7).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capsid assembly protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=57278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V120_HSV7J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422
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                                                        631 DNINSLTQTIFIPKTNFLVSLLLT-----AYTVHMQTYVNPWIQKTISENI-- 676
2 NEALMIL------SNGLLTYLTVLFLLFLFSKVSNVTLSKKELTLFSI------
                                                                                                                               NRRLLILIFACKLLMPSNYLLSH--YLLLLHAFT----LQIFKVDLGHFSIIHAITQKIF 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKGSNRGIGLAKVNHILEHYPKTSLQTS----NHHHLFKQLLIIK 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YETIKKI----NEYKEILESILIDKIYKIYTIHSKITNINAIINKLQNDKKH-----IH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LILFLILISFLS----QYTKQKVQNEI------MAQKEAQIRNITQYSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIFKPNFEKNKTILSLPRKALIRQMGINYIKSLGFDNISGSPIILKYKDVKKEKEYYNNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDTRYNIGHLANIQNDAVKGILSAKILEAQ -- NKKIAVNVEVSSKIQLPEMELLDFITIL 346
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 34, Created)
(Rel. 34, Last sequence up)
(Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -DIDNIRIYFKNIVEIYIPGVSLFPVKEIECEDKDVISILKNYMPSVGKSVIIF 421
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IRTYSKDLLQTTFKHINYQYLWEYILVFK 559
                                                                                             -SNFLIMIAVTMVNVNLFYPAEPLYFIALSIYLNR--QNSLSLNIFY 87
                                                                                                                                                                                                                                                                                                      110170 MW;
                                                                                                                                                                                                                           5.8%;
                                                                                                                                                                                                           70;
                                                                                                                                                                                                         Score 125.5; Pred. No. 2.5; 70; Mismatches
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                                                                                                                                                                                                                                                                                                      F4E39A2BF0D32BC9
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                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                           Indels 179;
                                                                                                                                                                                                                                             Length 938;
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RESULT SURA BEINT SURA
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                                                              Query Match
Best Local Similarity
Thehes 75; Conserv
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P57240;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-TOKYO 1998;

MEDLINE-20445173; PubMed=10993077;

Shigenobu S., Watanabe H., Ha'ttori M., Sakaki Y., Ishikawa H.;

"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";

Nature 407:81-86(2000).
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_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SURA OR BU140.
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16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
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                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP001118; BAB12858.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE PPIC/PARVULIN FAMILY OF ROTAMASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01096; PPIC_PPIASE_1; FALSE_NEG. PROSITE; PS50198; PPIC_PPIASE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro
                             168 LLYYLLIQVLYVIESYNVIPTLKFRKFVVIV----
                                                                                                                                                                                                                                                                                                                                                                                                   [somerase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           830 NFSLASQLIEA--KKLVKKQDTYNQLNVQD----DFVTVLKSHLNNLFEKQKPTINIERR 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 ---LSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILCDNAIEAAFESLNPEIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQIRNITQYSQQIESLYKDIRSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAFFKKNGSIVFIIONSTKEKOIDVSKIFKENY 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000297; Rotamase.
                                                                                                                                                                                                                                              179
286
430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Rotamase;
                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rotamase;
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                                                                                                                                                                                                                                 20 POTENTIAL.
430 SURVIVAL PROTEIN SURA HOM
277 PPIC 2.
386 PPIC 2.
50737 MW; CA4C425B3FBA5788 CRC64;
                                                                                                                   5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                   Repeat;
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                                                                                            55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                        Signal; Complete proteome. POTENTIAL.
                                                                                                                          Score 120.5;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                          SURVIVAL PROTEIN SURA HOMOLOG PPIC 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                            Mismatches
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                             ----YLILFL-----ILISFL 210
                                                                                                                                                     DB 1;
                                                                                            111;
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                                                                                                                                                 Length
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01-0CT-1996 (Rel. 34, Last sequ
01-NOV-1997 (Rel. 35, Last anno
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gardner M.J., Goldman N., Barnett P., Moore P.W., Rangachari K., Strath M., Whyte A., Williamson D.H., Wilson R.J.M.; "Phylogenetic analysis of the rpoB gene from the plastid-like DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BW(C10);
MEDLINE=95107345; PubMed=7808472;
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01-MAY-1991
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Pfam; PF00562; RNA_pol_B;
                       EMBL; X75544; CAA53232.1; -.
EMBL; X52177; CAA56427.1; -.
EMBL; X5275; CAA64572.1; -.
PIR; S10438; RNZQDE.
InterPro; IPR001572; RNA_Pol_B.
                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gardner M.J., Williamson D.H., Wilson R.J.M.;
"A circular DNA in malaria parasites encodes an RNA polymerase like that of prokaryotes and chloroplasts.";
Mol. Biochem. Parasitol. 44:115-124(1991).
-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THIS RNA POLYMERASE IS ENCODED ON A CIRCULAR DNA. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
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CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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Best Local
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P37873;
01-OCT-1994
 This
                                                          STRAIN-168 / JH642:
Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,
Sato T., Takeuchi M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REQUIRED FOR COMPLETE SEPTUM MIGRATION AND ENGULFMENT
                                                                                                                                                                             spolim
                                                                                                                                                                                                                                                                                          Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
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Transferase; Transcription; DNA-directed RNA polymerase.
SEQUENCE 1024 AA; 122185 MW; B49FBDED7C9BD412 CRC64.
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-93273731; PubMed-8501064;
Smith K., Bayer M.E., Youngman P.
                             OF THE FORESPORE COMPARTMENT DURING SPORULATION. -1- DEVELOPMENTAL STAGE: EXPRESSION STARTS 2 HOURS POST-SPORULATION.
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"Physical and
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                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                          Bacteriol.
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SWISS-PROT entry is copyright.
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                                                                                                                                                                                                       er M.E., Youngman P.;
functional characterization
                                                                                                                                                                          175:3607-3617(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --FLILISFLSQYTKQK-----VQNEIMAQKEAQIRNITQYSQQIE 241
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Pred. No. 7
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It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                 214
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YF02_AQUAE
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Best Local :
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067472;
16-0CT-2001
16-0CT-2001
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AQ_1502.
AQ_1502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: 4075
PIR: AA7581; A47581.
SubtiList; BG10768; spoIIM.
Subrulation; Complete proteome.
Sporulation; AA; 24296 MW;
                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                  Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L06664; AAA75553.1; -. EMBL; B4432; BAA12647.1; -. EMBL; D9416; CAB14285.1; -. PIR; A47581; A47581.
                  Hypothetical
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                                                 EMBL; AE000743; AAC07437.1; -
                                                                                                                                                                                                                                    Nature 392:353-358(1998).
                                                                                                                                                                                                                                                      aeolicus
                                                                                                                                                                                                                                                                                                                                                         STRAIN-VF5
                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Aquificales; NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                       MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 LLTYLTVLF---LLFLFSKVSNVTLSKKELTLFSISNFLIMI-----AVTMVNVNLFY
                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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52; Conser
l protein;
15 37
97 119
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                                Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                       Aquificaceae; Aquifex
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Pred. No. 1.
                  POTENTIAL.
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YC26_PORPU
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Best Local
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01-OCT-1996
01-OCT-1996
01-MAR-2002
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SEQUENCE
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Eukaryota; Rhodophyta;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypotherical sensor-like histidine kinase ycf26 (EC 2.7.3.-).
YCF26.
                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                  Plant Mol. Biol. Rep. 13:333-335(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-AVONPORT;
                         EMBL; U38804; AAC08278.1; -
                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
-!- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                   genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                  Reith M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2787;
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InterPro; IPR004358; BCTRLSENSOR.
                                                                                                                                                                                                                                                                                                                                                                                                             "Complet
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22.4%; Pr
tive 55;
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Best Local Similarity
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Pfam; PF00599; PAS; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00304; HAMP; 1.
SMART; SM00387; HATPASSE_C; 1.
SMART; SM00388; HISRA; 1.
SMART; SM00381; PAS; 1.
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InterPro; IPR003661; I
InterPro; IPR000014; I
Pfam; PF00672; HAMP; ]
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ransmembrane;
 TGLGLSIVKNIIQKH-----NSEIHLYSEL
                                                                                                                                                                     TSLR-LGIENKDLASIEKIYHQILEKTGHQLQDTRYNIGHLANIQND------A
                                                                                                                                                                                             GIAMTIQDRTQEVELNEIKNQ-----FISNVSHELRTPLFNIRSFLETLYEYHDSLDDS
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                      RGIGLAKVNHILEHYPKTSLQTSNHHHLFKQL 437
                                               IILRAYTVDDLKTETEVQHFNSQKVRVEICDNGIGISRKNQERIFARFLRIENYVHTLEG
                                                                      ----AFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFK----ENYSTKGSN
                                                                                              VEQTIRTYQLSAKDKRIDLHIDIEQNLQ---CVLGNYNLILQILANLVVNSLKFTHPNGI 55
                                                                                                                     VKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILCDNAIEA-----
                                                                                                                                              QKLEFLAIANKETGRLTRLVNDVLD-------LSRLESDQEYTLQPTDLVSA
                                                                                                                                                                                                                  -ISFLSQYTKQKVQ-NEIMAQKEAQIRNITQYSQQIESLYKDIRSE-----RHDYLNIL 258
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PS50112; PAS; 1.
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IPR003594;
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His_kinA.
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HISTIDINE KINASE.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
2B3DDE7C91AEE680 CRC64;
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Search completed: July 30, Job time: 365 sec 2002, 15:20:54

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Result
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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     749
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517
455
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebra

6: sp_mammal:*

7: sp_mammal:*

8: sp_organelle

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebra

14: sp_unclass:*

15: sp_bacteria:

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17: sp_bacteria:
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2173
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_phage:*
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sp_virus:*
sp_vertebrate:*
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Q9s115 streptococc
Q9s135 streptococc
Q9s137 streptococc
Q99yp4 streptococc
Q99yp4 streptococc
Q99mw1 clostridium
P95767 streptococc
Q97a446 streptococc
Q33597 streptococc
Q33597 streptococc
Q3x995 streptococc
Q3x995 streptococc
Q3x995 streptococc
Q3x995 streptococc
Q3x996 streptococc
Q3x916 streptococc
Q3x916 streptococc
Q3x916 streptococc
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Q9f2f5 streptococc
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45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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## ALIGNMENTS

SRESULT 1  OSPERE: DO OSPERE: DI -MAR-2001 (TrEMBLITEL 16, Created) DT 01-MAR-2001 (TrEMBLITEL 16, Last sequence update) DT 01-MAR-2001 (TrEMBLITEL 19, Last annotation update) DE HISTIDINE KIRASE.  OS Streptococcus pneumoniae. OS Streptococcus pneumoniae. OS Streptococcus pneumoniae. OS STRAIN-SP670; RI 11 11 11 11 11 11 11 11 11 11 11 11 11	~	-	_		70	**		-	_	_	_	-1	74	131	•==	<b>T</b>	-	חבי	7	0	0	0	0	0		ь	_		4	<b>-</b>	2	<b>2</b> 11
99F2F2  PRELIMINARY; PRT; 446 AA.  99F2F2  PRELIMINARY; PRT; 446 AA.  99F2F2  1 -MAR-2001 (TrEMBLrel. 16, Last sequence update)  11 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  12 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  13 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  14 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  15 -EQUENCE FROW N.A.  16 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  16 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  18 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  18 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  19 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  10 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  10 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  11 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  12 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  13 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  14 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  15 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  16 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  17 -DEC-2002 (TrEMBLREL 19, Last sequence update)  18 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  19 -DEC-2001 (TrEMBLrel. 19, Last sequence update)  10 -DEC-2002 (TrEMBLREL 19, Last sequence update)  10 -DEC-2002 (TrEMBLREL 19, Last sequence update)  11 -DEC-2002 (TrEMBLREL 19, Last sequence update)  12 -DEC-2002 (TrEMBLREL 19, Last sequence update)  13 -DEC-2002 (TrEMBLREL 19, Last sequence update)  14 -DEC-2002 (TrEMBLREL 19, Last sequence update)  14 -DEC-2002 (TrEMBLREL 19, Last sequence update)  16 -DEC-2002 (TrEMBLREL 19, Last sequence update)  17 -DEC-2002 (TrEMBLREL 19, Last sequence update)  18 -DEC-2002 (TrEMBLREL 19, Last sequence update)  19 -DEC-2002 (TrEMBLREL 19, Last sequence update)  10 -DEC-2002 (TrEMBLREL 19, Last sequence update)  10 -DEC-2002 (TrEMBLREL 19, Last se	у	ğ	Ϋ́	Qu Ma	ŏ	Ê	ਝੱ	<b>∞</b> ∶	Ħ	Ħ	Ħ	Ã	ã	ã	õ	×	റ്	õ	ž	×	ი ი	റ്	õ	Ż	Ħ	Ä	Ä	ĕ	S	Ö	9F2	ESU
	55 V-NVNLFYPAEPLYFIALSIYLNRQNSLSLNIFYGILPVASSDLFRRAIIFFILDGTQ 111		- <b>द</b>	35.6%; Score 773; DB 2; Length 446; Similarity 38.8%; Pred. No. 5.4e-37; 4; Conservative 91; Mismatches 168; Indels 16; Gaps	446 AA; 52057 MW;		PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.	SMART; SM00387; HATPASE_C; 1	InterPro: IPR003594; HATPase_c.	InterPro; IPR001064; Crystallin.	EMBL; AJ278302; CAC10175.1;	FEMS Microbiol, Lett. 190:231-236(2000).				MEDLINE=20487097; PubMed=11034284;	STRAIN=SP670;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=1313;	Streptococcus.	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;	Streptococcus pneumoniae.	IH.	HISTIDINE KINASE.	BLrel. 19,	(TrEMBLrel. 16,	(TrEMBLrel. 16,	Q9F2F2;	PRELIMINARY; PRT;	่งั่	נת 1

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Best Local
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FEMS Microbiol. Lett. 190:231-236(2000)
EMBL; AJ278301; CAC10171.1; -.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                        InterPro; IPR001064; Crystallin.
InterPro; IPR003594; HATPase_c.
SMART; SM00387; HATPase_c; 1.
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                                                                                                                                                                                                                                             PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
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Wallelic variation in a peptide-inducible
117
                       115
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                       --MGSSIITTYMIEFAGIALSYLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITMLLYYL 172
                                                  SKYLSYFIEPLFGIGLSFLLLRGLPKKILIFYGLFPMILVELFYRGVSYFVLPFLGQGIV
                                                                         NVNLFYPAEPLYFIALSIYLNRQNSLSLNIFYGLLPVASSDLFRRAIIFFILDGT-QGIV 114
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                                                                                                                                                       Score 755; DB 2;
Pred. No. 5.8e-36;
38; Mismatches 171;
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Last annotation updat
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HISTIDINE KINASE (BLPH PPOTATIVE).
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Q1-MAY-2000
Q1-MAY-2000
Q1-OCT-2001
Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heldelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Galnn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus Science 293:498-506(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reichmann P., Hakenbeck R.; "A Peptide Inducible Signal Transduction System in Streptococcus pneumoniae: Evidence for Bacteriocin Production."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=99453779; PubMed=10524254;

Lange R., Wagner C., de Salzleu A.B., Flint N., Molnos (Caspers P., Kamber M., Keck W., Amrein K.;

"Domain organization and molecular characterization of Component systems identified by genome sequencing of S. Gene 237:223-234(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                          de Saizieu A., Gardes C., Flint N., Wagner C., Mitchhell T.J., Keck W., Amrein K.E., Lange R.; "Microarray based identification of a novel Streegulon controlled by an autoinduced peptide."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ c
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Best Local
                                                                                                                                                                                                                                                                                                    032832;
                                        Stephens S.K., Floriano B., Cathcart D.P., Bayley Jimenez-Diaz R., Warner P.J., Ruiz-Barba J.L.;
"Molecular analysis of the locus responsible for plantaricin S, a two-peptide bacteriocin produced plantarum LPCO10.";
                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE HISTIDINE KINASE (EC 2.7.3.-) (ORF8).
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 EMBL; Y15127; CAA75398.1;
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AJ278419;
AJ276410;
AE007364;
SP0527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.5%; Score 749; DB 16; 37.8%; Pred. No. 1.3e-35;
                                                                                                                                                                                                    Bacillus/Clostridium group;
                               64:1871-1871(1998)
              INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89;
                                                                                                                                                                                                                                                                                                                  PRT;
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InterPro; IPR004359; HIS_KIN_sig.
Pfam; PF02518; HATPase_c; 1.
             STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
MEDLINE=21192694; PubMed=11296296;
Ferretti J.J. McShan W.M. Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Frimeaux C., Sezate S., Suvozov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
EMBL; AE006491; AAK33320.1; -.
                                                                                                                                                                                                          SPY0242.
Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
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InterPro; IPR003594; HATPase_c.
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=1314;
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Best Local
                                                                                     STRAIN-SF370 / ATCC 700294 / SEROTYPE M1;
MEDLINS-21192684; PubMed=11296296;
MEDLINS-21192684; PubMed=11296296;
MEDLINS-21192684; PubMed=11296296;
MEDLINS-21192684; PubMed=11296296;
MEDLINS-21192684; Pavic G., Lyon K.,
Ferretti J.J., McShan W.A., Addic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL; AE006592; ARX14382 1; -.
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Kinase; Complete proteome.
SEQUENCE 448 AA; 52221 MW; 230C003A104CBEF5
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Pfam; PF02518; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
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                                                          Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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5; Mismatches 173;
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          045D080E66D45B97 CRC64;
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5 LMILSNGLLTYLTVLFLLF-LFSKVSNVTLSKKELTLFSISNFLIMIAVTMVNVNLFYP-

Matches 122;

Conservative

110; Mismatches

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Indels

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MMVIYSMALFYATIFINSWVIFAKVSAIKLSWKRVSI-

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Best Local Similarity
                                                                                                                                                                                           STRAIN-SF370 / ATCC 700294 / SEROTYPE M1;

MEDLINB-21192684; pubmed=11296296;

Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,

Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.",

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                   Kinase; Complete proteome. SEQUENCE 427 AA; 49908 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1314;
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   Local Similarity
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23.8%;
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Pred. No. 8e-23;
Score 517; DB 16;
Pred. No. 2.5e-22;
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                                                                                                                                          01C9D236E4D7A0D6 CRC64;
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Best Local :
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MEDLINE-2139325; PubMed-11466286;

Noelling J. Breton G. Omelchenko M.V. Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

J. Bacteriol. 18134823-4818(2001).

EMBL, AE007529; AAK/8065 1;

EMBL, AE007529; AAK/8065 1;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HISTIDINE KINASE-LIKE ATPASE;
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SMART; SM00387; HATPase_c; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1488;
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121 -TTYMIEFAGIALSYLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITMLLYYLLIQVLYV 179
                                                                         71 LSIYLNRQNS---LSLNIFYGLLPVASS-----DLFRRAIIFFILDGTQGIVMGSSII- 120
                                                                                                                33 GMIVITEIISLIFLM-----LGWQQVTVMA---
                                                                                                                                                      11 GLLTYLTVLFLLFLFSKVSNVTLSKKELTLFSISNFLIMIAVTMVNVNLFYPAEPLYFIA 70
                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 ---AEPLYFIALSIYLNRQNSLSLNIFYGLLPVASSDLFRRAIIFFILDGTQGIVMGSSI 119
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                                     PCIFMYLQTSDVVLSIS-----LPVAGCLIIIVWDYFLSVLYNYVFLVNQSVIKNDVSIH 116
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                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                        20.9%; Score 455; DB 16; 27.4%; Pred. No. 9.4e-19;
                                                                                                                                                                                       96; Mismatches 163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 AA.
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EMBL; U80077; AAC45306.1; -.
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Lunsford R.D., Roble A.G.;
"comYA, a gene similar to comGA of Bacillus subtilis, is essential for
competence-factor-dependent DNA transformation in Streptococcus
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01-MAY-1997 (TrEMBLREL. 03, Last sequence update)
01-DEC-2001 (TrEMBLREL. 19, Last annotation updat
HISTIDINE PROTEIN KINASE.
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                                                                                                                                                                                 175 QVLY-----VIESY-NVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKE 227
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STRAIN-CHALLIS (NCTC 7868);
MEDILINE-97032151, PubMed-8878047;
MEDILINE-97032151, PubMed P., Nes I.F., Morrison D.A.;
"Identification of the streptococcal competence-pheror Mol. Microbiol. 21:863-869(1996).
MEMBL: X98109; CAA66787.1; ...
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                                                                                                                                               AQIRNITQYSQQIESLYKDIRSFRHDYLNILTSLRLGIENKDLASIEKIYHQILEKTGHQ
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                                                                                                                                                                                                                                                                                                                     FYPAEPLYFIALSIYLNRQNSLSLNIFYGL---LPVASSDLFRRAIIFFILDGTQGIVMG
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IGLAKVNHILEHYPKTSLQTSNHHHLFKQLLIIK 441
                           VLLNNAVEGAAESPSKTMNVSLVKLDKETVFVIQNSRQSRYINLEEIYEVGFSTKGENRG
                                                                               LRSDDYTFFELNNVQDTALRSVLIQTIFKARECGVEIVFEMKDVIETLPMKLLDLVRVAS
                                                                                                         LODTRYNIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILS
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                                                                                                                                                                                                                                            DSFVKQHYDIFYIIINLLSLFIILKVVDFFDFYFEYYKEPIYKNDLYNVNKSYIVIHILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53633 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                      94;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 450; DB 2;
Pred. No. 1.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281D55CDFE4063E2
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       competence-pheromone receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453
                                                                                                                                                                                                                                                                                                                                                                                                      180;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                              414
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RESULT
033597
ID 03
AC 03
DT 01
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Best Local
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O33646;
O1-JAN-1998
O1-JAN-1998
O1-DEC-2001
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SEQUENCE
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01-DEC-2001 (TrEMBLrel.
HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=NCTC 3155;

MEDLINE=98012933; PubMed=9352904;

Havarstein L.S., Hakenbeck R., Gaustad P.;

"Natural competence in the genus Streptococcus: Evidence that

"Natural competence in the genus Streptococcus: Evidence that
streptococci can change pherotype by interspecies recombinational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus gordonii.
Bacteria; Firmicutes; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exchanges.";
J. Bacteriol. 179:6589-6594(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLTYLTVLELLFLFSKYSNYTLSKKELTLFSISNFL--IMIAVTMVNVNLEYPAEPLYFI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFLYLTISFSSLILTQFYNLLPEYGDV----LSTFLHYLLIFFQPLILHLYFSKKGLYKG 93
                                                                                         NVKETIDKYDEVILETDIETNYFIQVVRFK
                                                                                                      KVNHILEHYPKTSLQTSNHHHLFKQLLIIK 441
                                                                                                                                                                                                                                                                                                                                                                                                        YVSIF-----LSLLIY----LSVSSSETFFSVII------SSVTGDDFVNQYWGSYYT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                ALSIYLNRONSLSLNIFYGLLPVASSDLFRRAIIFFILDGTQGIVMGSSIITTY ----- 123
                                                                                                                                            NAVEGAAESPSKTMNVSLVKLDKEIVFVIQNSRQSRYINLEEIYEVGFSTKGENRGLGLN
                                                                                                                                                                    NAIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIGLA 411
                                                                                                                                                                                             DYTFFELNNVQDTALRSVLIQTIFKARECGVEIVFEMKDVIGTLPMKLLDLVRVASVLLN
                                                                                                                                                                                                                       RYNIGHLANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILCD
                                                                                                                                                                                                                                                 QLQLYTDEIVGLYNEIRGFRHDYAGMLTSLQTGINSGDMKEVERIFHNVLSQANISLRSD
                                                                                                                                                                                                                                                                                                                        LLIQVLYVIESYNVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQIR 231
                                                                                                                                                                                                                                                                                                                                                    IVNILALFFYLKSFEFFEFEFSYFKNFDFEKEI.-----MNVIKIYVTIHILLNISH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                             --MIEFAGIALSYLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITMLLYY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAA04357.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52756 MW;
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Last annotation update)
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033597; 01-JAN-1998 (TrEMBLrel. 05,

Created)

033597

PRELIMINARY;

PRT;

448

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RESULT 13
Q9X995
ID Q9X995
AC Q9X995
DT 01-NOV
DT 01-EC
COMD P
GN COMD P
GN COMD P
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GN COMD P
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Best Local S
Matches 105
                                                              Q9x995
Q9x995;
Q1-NOV-1999
Q1-NOV-1999
Q1-DEC-2001
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Havarstein L.S., Hakenbeck R., Gaustad P.;
"Natural competence in the genus Streptococcus: Evidence that
streptococci can change pherotype by interspecies recombinational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus
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01-DEC-2001 (TrEMBLrel.
HISTIDINE KINASE.
Streptococcus oralis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 179:6589-6594(1997).
EMBL; AJ000864; CAA04342.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exchanges.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-NCTC 10713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003594; HATPase_c.
InterPro; IPR004359; HIS_KIN_sig.
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                                                 PROTEIN
                                                                                                                                                                                                    NNYEGIILDTKIEDEYFTQVMRVR 436
                                                                                                                                                                                                                                                             AESYQKTMNVSLVDLDTETTLVIQNSRKKRPLDLEEIYQTDFSTKGEGRGLGLSNIKEII
                                                                                                                                                                                                                                                                                                                                                   LANIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILCDNAIEAA
                                                                                                                                                                                                                                                                                                                                                                                 DETYSLYNEIRGFRHDYGGMLASFQSAIHTGDIKEVERIYQEVLVNANLQLRSDKYTYFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GLFYIFINIISLVFILKAİDYFKFNFKYFKKIDFKENIVQLNFYLLFIHLLLNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y-LYFFKVKKVKKHLSVFLALFLSLAVSSSETFFSVII-----SSVTGDKFVDRYW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IALSIYLNRQNSLSLNIFYGL---LPVASSDLFRRAIIFFILDGTQGIVMGSSIITTYMI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFSIIEAVSVVYCYKKISRVNKVNIHFTLLCLGIVFSTDFTTLIHYSIRYMMFFIQPLFF
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                                                                                                                                                                                                                               EHYPKTSLQTSNHHHLFKQLLIIK 441
                                                                                                                                                                                                                                                                                        FESLIPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIGLAKVNHIL 417
                                                                                                                                                                                                                                                                                                                        LNNVGDSALRSVMTQTLFKTRDYNIELTFEVKDFVNPLPIKLLDLVRMTSVLLNNAIEGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVIESYNVIPTLKERKEVVIVYLILELILISELSQYTKQKVQNEIMAQKEAQIRNITQYS
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                                                              (TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52922 MW;
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Last anno
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annotation update)
                                                                 annotation
                                                                            sequence update)
                                                                                                                          441 AA.
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RESULT
Q9X990
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Best Local
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Mol. Ecol. 8:2033-2035(1999).
EMBL; AJZ404794; CAB39420.1; -
InterPro; IPR004359; HIS_KIN_s1g.
SEQUENCE 441 AA; 51328 MW; 63AC032CAA3DEC9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-COL19;
                                                                                         Q9X990;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whatmore A.M.; "Genetic diversity of the streptococcal competence (com) locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus.
NCBI_TaxID=1303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20098376; PubMed=10632854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=COL19
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NCBI_TaxID=28037;
                                                                   COMD.
                                                                               COMD PROTEIN.
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                      Streptococcus
                                      Bacteria; Firmicutes;
                                                    Streptococcus mitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 LSLNIFYGLLPVASSDLFRRAIIFFILDGTQGIVMGSSIIT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 LSKKELTLFSISNFLIMIAVTMVNVNLFYPAE-----PL----YFIALSIYLNRQNS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 IKSKELYFFGIYTLLVE-AVLELSFYLLYLDEIVIERFLFPLGLYSYFRWIKQY-ERDRG 85
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                                                                                                                                                                                                                     ILETEMEGSTFRQIIRFK 437
                                                                                                                                                                                                                                               SLQTSNHHHLFKQLLIIK 441
                                                                                                                                                                                                                                                                          QMEVAVIKMETETVIVIQNSCKMTMTPSGDLFALGFSTKGRNRGVGLNNVKELLDKYNNI 419
                                                                                                                                                                                                                                                                                                     EIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIGLAKVNHILEHYPKT
                                                                                                                                                                                                                                                                                                                               SALRSLVAQSIVYARNNGVEFTLEVKDTITKLPIELLDLVRIMSVLLNNAVEGSADSYKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGIALSYLFLSVFNVDIGRLKDSLTKMKVKKRLIPMNITMLLYYLLIQVLYVIESYNVIP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                          TIRHLNSFGSILSSIVFISLLLTFFAMNSHKEQMEKEIALKQKKFEQKHLQNYTDEIVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLK-FRKFVVIVYLILF--LILISFLSQYTKQKVQNEI-MAQKEAQIRNITQYSQQIESL 243
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121; Conserva
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                                                                                                                                                  PRELIMINARY;
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27.6%; Pred. No. 7.1
                                        Bacillus/Clostridium group; Streptococcaceae;
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                                                                                            Last sequence update)
Last annotation updat
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RESULT 15
P72444
ID P72444
AC P72444
AC P72444
AC P72444
DT 01-FEB
DT 01-FEB
DT 01-DEC
DE HISTID
GN COMD2.
OS Strept
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Best Local Similarity
Matches 119; Conserv
                                                                      Streptococcus gordonii.
Bacteria; Firmicutes; B
Streptococcus.
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01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Mol. Ecol. 8:2023-2035(1999).

EMBL; AJZ40795; CAB39417.1; -.

InterPro; IPRO04359; HIS_KIN_sig.

SEQUENCE . 441 AA; 51291 MW; 94FB
 SEQUENCE FROM N.A. STRAIN=NCTC 7865; MEDLINE-97032151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=NCTC10712;
MEDLINE=20098376; PubMed=10632854;
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                                                        NCBI_TaxID=1302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSLD------GLGIVTFLFPLGLYSYFRWIKQYERDRGLFLSLLLSLLYESTHNFLS 104
                                                                                                                                                                                                                                                                                                                                EVKDTITELSIELLDLVRIMSVLLNNAVEGSADSYKKQMEVAVIKMDVETVIVIQNSCKM
                                                                                                                                                                                                                                                                                                                                                          EVSSKIQLPEMELLDFITILSILCDNAIEAAFESLNPEIQLAFFKKNGSIVFIIQNSTKE
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   PubMed=8878047;
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19,
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1%; Pred. No. 8.1e-18;
102; Mismatches 165;
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                                                                                   group; Streptococcaceae;
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EMBL; x98110; CAA66789.1; ".
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                                                                                                                                NIQNDAVKGILSAKILEAQNKKIAVNVEVSSKIQLPEMELLDFITILSILCDNAIEAAFE
                                                        SPSKTMNVSLVKLDKEIVFVIQNSRQSRYINLEEIYEVGFSTKGENRGLGLNNVKEIIDK 425
                                                                           SLNPEIQLAFFKKNGSIVFIIQNSTKEKQIDVSKIFKENYSTKGSNRGIGLAKVNHILEH
                                                                                                                                                                           IVGLYNEIRGFRHDYAGMLISLQTGINSGDMKEVERIFHNVLSQANISLRSDDYTFFELN
                                                                                                                                                                                                                                                                                                                          -----FAGIALSYLFLSVFNVDIGRLKDSLTKMKV-KKRLIPMNITMLLYYLLIQVLYV 179
YDEVILETDIETNYFIQVVRFK
                            YPKTSLQTSNHHHLFKQLLIIK 441
                                                                                                                 NVQDTALRSVLIQTIFKARECGVETVFEMKDVIETLPMKLLDLVRVASVLLNNAVEGAAE
                                                                                                                                                                                             IESLYKDIRSERHDYLNILTSLRLGIENKDLASIEKTYHQILEKTGHQLQDTRYNIGHLA
                                                                                                                                                                                                                                   FSENAHLNS--FASMIATIGFIMFLSTLFYLKSAREQHEKAKEIQQKKEEQRQLQLYTDE
                                                                                                                                                                                                                                                                  IESYNVIPTLKFRKFVVIVYLILFLILISFLSQYTKQKVQNEIMAQKEAQIRNITQYSQQ
                                                                                                                                                                                                                                                                                               QHYDIFYIIINLLSLFIILKVYDFFDFYFXYYKEPIYKNDLYNVNKSYIVIHILLNISHW
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119; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 437; DB 2;
Pred. No. le-17;
7; Mismatches 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184;
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Search completed: July 30, 2002, 15:20:32 Job time: 378 sec